

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame.p1us.p2n model

Run on: December 22, 2005, 00:16:14 ; Search time 983 Seconds

(without alignments)
4382.854 Million cell updates/sec

Title: US-09-857-581B-66

Sequence: 1 MLELALGLXVIALFYHLRP.....ASHLVCPLARIGVASKLS 521

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODE=frame+ p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO.epool_p/US09857581/runat_15122005_083138_19431/app_query.fasta_1.711
-DB=Published Applications NA_Main -QPM=fastlap -SUFFIX=rnpbm -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blonum62
-TRNS=human40.cdt -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09857581 @CGN_1.1.1549 @runat_15122005_083138_19431
-NCPU=6 -ICPU=3 -NO MAP -LARGQUERY -NEG_SCORES=0 -WAIT -DSBBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Published Applications NA_Main:

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 2258 | 94.5 | 1756 | 6 | US-10-171-174A-9* |
| 2 | 2258 | 94.5 | 1756 | 6 | US-10-104-706-1* |
| 3 | 2256 | 94.4 | 1709 | 6 | US-10-310-154-367 |
| 4 | 2256 | 94.4 | 1709 | 6 | US-10-732-923-309 |
| 5 | 2250 | 94.2 | 1824 | 7 | US-10-659-755-1 |
| 6 | 2248 | 94.1 | 1567 | 9 | US-10-505-145-3 |
| 7 | 2130 | 89.2 | 1974 | 8 | US-10-739-930-3497 |
| 8 | 944.5 | 39.5 | 1730 | 6 | US-10-411-115-3 |

| | | | | | | |
|----|-------|------|------|---|----------------------|--------------------|
| 9 | 944.5 | 39.5 | 1730 | 8 | US-10-411-225-3 | Sequence 3, Appli |
| 10 | 943.5 | 39.5 | 1724 | 6 | US-10-411-115-1 | Sequence 1, Appli |
| 11 | 943.5 | 39.5 | 1724 | 6 | US-10-411-225-1 | Sequence 1, Appli |
| 12 | 921.5 | 38.6 | 1770 | 8 | US-10-411-115-7 | Sequence 7, Appli |
| 13 | 921.5 | 38.6 | 1770 | 8 | US-10-411-225-7 | Sequence 7, Appli |
| 14 | 919.5 | 38.5 | 1841 | 7 | US-10-424-599-6882 | Sequence 6882, Ap |
| 15 | 877.5 | 36.7 | 1328 | 7 | US-10-424-599-78567 | Sequence 78567, A |
| 16 | 870 | 36.4 | 1842 | 7 | US-10-424-599-10588 | Sequence 10588, |
| 17 | 843 | 35.3 | 1506 | 7 | US-10-424-599-101968 | Sequence 101968, |
| 18 | 807.5 | 33.8 | 1740 | 7 | US-10-437-963-48274 | Sequence 48274, A |
| 19 | 761.5 | 31.9 | 1650 | 7 | US-10-437-963-21012 | Sequence 21012, A |
| 20 | 730.5 | 30.6 | 1893 | 7 | US-10-437-963-67133 | Sequence 67133, A |
| 21 | 717 | 30.0 | 2278 | 7 | US-10-424-599-100510 | Sequence 100510, |
| 22 | 701.5 | 29.4 | 1719 | 7 | US-10-424-599-115417 | Sequence 115417, |
| 23 | 693 | 29.0 | 1308 | 7 | US-10-260-238-1264 | Sequence 1264, Ap |
| 24 | 691.5 | 28.9 | 1825 | 7 | US-10-425-114-24949 | Sequence 24949, A |
| 25 | 680.5 | 28.5 | 1915 | 8 | US-10-425-115-89837 | Sequence 89837, A |
| 26 | 680.5 | 28.5 | 2233 | 8 | US-10-739-930-2248 | Sequence 2248, Ap |
| 27 | 666.5 | 27.9 | 1930 | 8 | US-10-425-115-94744 | Sequence 94744, A |
| 28 | 657 | 27.5 | 1633 | 7 | US-10-437-963-38374 | Sequence 38374, A |
| 29 | 651 | 27.2 | 1530 | 6 | US-10-097-559-12 | Sequence 12, Appli |
| 30 | 649.5 | 27.2 | 1922 | 7 | US-10-425-114-27875 | Sequence 27875, A |
| 31 | 649.5 | 27.2 | 2008 | 8 | US-10-425-115-94743 | Sequence 94743, A |
| 32 | 637.5 | 26.7 | 1660 | 9 | US-10-669-962-16 | Sequence 16, Appli |
| 33 | 637 | 26.7 | 5822 | 7 | US-10-437-963-3724 | Sequence 3724, Ap |
| 34 | 634 | 26.5 | 1615 | 7 | US-10-686-947-259 | Sequence 259, App |
| 35 | 634 | 26.5 | 1615 | 9 | US-10-943-507-254 | Sequence 254, App |
| 36 | 633.5 | 26.5 | 1610 | 7 | US-10-686-947-197 | Sequence 197, App |
| 37 | 633.5 | 26.5 | 1610 | 9 | US-10-686-947-261 | Sequence 261, App |
| 38 | 633.5 | 26.5 | 1610 | 9 | US-10-943-507-194 | Sequence 194, App |
| 39 | 633.5 | 26.5 | 1610 | 9 | US-10-943-507-256 | Sequence 256, App |
| 40 | 632.5 | 26.5 | 1657 | 7 | US-10-686-947-195 | Sequence 195, App |
| 41 | 632.5 | 26.5 | 1657 | 9 | US-10-943-507-192 | Sequence 192, App |
| 42 | 631 | 26.4 | 1652 | 7 | US-10-686-947-193 | Sequence 193, App |
| 43 | 631 | 26.4 | 1652 | 9 | US-10-943-507-190 | Sequence 190, App |
| 44 | 631 | 26.4 | 1862 | 7 | US-10-437-963-46212 | Sequence 46212, A |
| 45 | 630.5 | 26.4 | 2081 | 7 | US-10-424-599-2618 | Sequence 2618, Ap |

ALIGNMENTS

RESULT 1
US-10-171-174A-9
; Sequence 9, Application US/10171174A
; Publication No. US20030150012A1
; GENERAL INFORMATION:
; APPLICANT: Odell, Joan
; APPLICANT: YU, Xiaodan
; TITLE OF INVENTION: A METHOD FOR ALTERING THE ISOFLAVONOID PROFILE IN THE PLANT PART
; FILE REFERENCE: B81452 US NA
; CURRENT APPLICATION NUMBER: US/10/171,174A
; PRIOR FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: 60/297,981
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 9
; LENGTH: 1756
; TYPE: DNA
; ORGANISM: Glycine max
US-10-171-174A-9

Alignment Scores:

Pred. No.: 0
Score: 2258.00
Percent Similarity: 86.76%
Best Local Similarity: 86.76%
Query Match: 94.52%
DB: 6
US-09-857-581B-66 (1-521) x US-10-171-174A-9 (1-1756)

Length: 1756
Matches: 452
Conservative: 0
Mismatches: 69
Indels: 0
Gaps: 0

QY ThrPro***Ala***SerIysAlaLeuArgHISLeuProAsnProProSerPro***Pro 40
 DB 127 ACACCAAGGCAAAATCAAAAGACACTTCGCCACCTCCAAACCTCCAAAGCCCAAGCCCT 186
 QY ArgLeuProPheIleGlyHis***HisLeuLeuAspLysLeuLeuHISLysAla*** 60
 DB 187 CGCTCCCTTCATTTGGCCACCTTCACCTCTTAAAGATAACTTCTCCACTATGCACTC 246
 QY 11LeuPleuSerLysLysHisGlyProLeuPheSer*****PheGlySerMetProThr 80
 DB 247 ATCGATCTCTCCAAAAGAGAGCCCTTATCTCTCTCTCTCCGCTCCATGCAAC 306
 QY 81ValValAlaSerThrProGluLeuPheLysLeuPheLeuGln*****GluAlaThrSer 100
 DB 307 GTCTGTGCTCCACCCCTGAGTTGTTCAAGCTCTTCTCCAAACCAAGCAAGCACTTC 366
 QY Phe***ThrArgPheGlnThrSerAla***Arg***LeuThrTyraSp*****ValAla 120
 DB 367 TTCACACAAAGTTCCAAACCTCTGCCATTAAGAGCCCTCACTACGAACTCTGTGGCC 426
 QY 121*****Pro***GlyProTyraSp***PheValArgLysLeuIleMetAsnAspLeu*** 140
 DB 427 ATGGTTCCATTCCGACCTTAAGTGAAGTTCTGAGAGAGCTCATGAACGACCTTCTC 486
 QY 141AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***Leu 160
 DB 487 AACGCCAACCCCTCAACAAAGCTCAGGCCCTTGAAGACCAACAAAGATCCGCAAGTTCC 546
 QY 161Arg***MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGluLeuLeu 180
 DB 547 AGGGTATAGCCCAAGAGCCGAGAGCCCAAGAGCCCTTACGCTCAAGGAGACTTCTC 606
 QY 181LysTyr***AsnSerThr***SerMetMet***LeuGlyGluAlaGluGluIleArgAsp 200
 DB 607 AATAGGCAACCAAGCAACATCTCATGATGATGCTCGCAGAGCTGAGGAGATCAGAC 666
 QY 201IleAlaArgGluValLeuLysIle***GlyGluTyraSerLeuThrAspPheIle***Pro 220
 DB 667 ATGCTTCGCAAGGTTCTTAAGATCTTGGCGAATACAGCTCCTCACTGACTTCACTGGCCT 726
 QY 221LeuLys***LeuLysValGlyLysTyraGluLysArgIleAspAspIleLeuAsnLysPhe 240
 DB 727 TTGAAGATATCTCAAGTTGGAAGTATGAGAAGAGATGATGATGATGATGATGATGATG 786
 QY 241AspProValValGluArgValIleLysLysArgArg***IleValAlaGlyArg***Asn 260
 DB 787 GACCTGTCTGTTAAAGGTCATCAGAGAGGCGCTGAGATCTGCAAGAGAGAGAAAGAC 846
 QY 261GlyGlu*****GlyGlyGlu***SerGlyVal***LeuAspThrLeuLeuGluPheAla 280
 DB 847 GGAAGATGTTGTTGAGGCGAGGCGAGGCGCTCTCTCCAGACCTTGTGTTGATTTGCT 906
 QY 281GluAspGluThr***GluIleLysIleThrLys*****Ile***GlyLeuValValAsp 300
 DB 907 GAGACGAGACCAATGAGATCAAAATTAACAAAGAGCAAAATCAAGGCTTGTGTGCAC 966
 QY 301***PheSerAlaGly***AspSerThrAla*****ThrGluTyrPalaleuAlaGluLeu 320
 DB 967 TTTTCTCTGCAAGGAGCATTTCCACAGCGGTGCAACAGAGTGGGCACTTGGCAGACTC 1026
 QY 321IleAsnAsnPro***ValLeu*****AlaArgGluGlu***TyrSerValValGlyLys 340
 DB 1027 ATCAACAAATCCAGAGGTTGTTCAAAAAGCTCTGAGAGAGCTTCAAGTGTGTGGCAAA 1086
 QY 341Asp***LeuValAspGluValAspThrGlnAsnLeuProTyraArgAlaIleValLys 360
 DB 1087 GATGAGACTGTTGAGCAAGTTGACACTCAAAACCTTCACTTACATTAAGGCGCATTTGTGA 1146
 QY 361GluThrPheArgMetHisProProLeuProValValLysArgLysCys***GluGluCys 380
 DB 1147 GAGACATTCCGAATGCAACCACTCCAGGAGGCAAAAGAGTGCACGAAGAGTGT 1206
 QY 381***IleAsnGly***Val***ProGluGlyAlaLeu*****PheAsnValTyrGluVal 400

DB 1207 GAGATTAATGGGTATGATATCCAGAGGAGCATTTGTTCTTTCAATGTTTGGCAAGTA 1266
 QY 401 Gly***Asp***LysTyraTyrAspArgProSerGlu***ArgProGluArgPheLeuGlu 420
 DB 1267 GGAAGGAGACCCCAAAATACGGGAGAGACATCAGAAATCCGTCAGAGAGGTTCTTAGAA 1326
 QY 421 Thr***AlaGluGlyGluAla*****LeuAspLeuArgGly***HisPheGlnLeuLeu 440
 DB 1327 ACTGTGCTGAAGGGGAGAGAGGCGCTCTGTATCTTAAGGGCCAGCATTTCAACTCTC 1386
 QY 441 PropheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***Ala 460
 DB 1387 CCATTGGGTCTGGAGAGAGATGTCCTGTGTGTCATTTGGCTACTTCAGAGATGCA 1446
 QY 461 ThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGln 480
 DB 1447 ACACCTCTTGACATCTTATCCAAATGCTTTGACCTGCAAGTCTGGGCCCTCAAGGACA 1506
 QY 481 IleLeuLysGly***AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValPro 500
 DB 1507 ATATTGAAGGTGATGATGATCCAAAGTTAGCATGAGAAAGAGAGCTGGCTCAAGTTCA 1566
 QY 501 ArgAlaHisSerLeuValCysValProLeuAlaArgIleGlyValAlaSerLysLeuLeu 520
 DB 1567 AGGGCACAATGATCTCGTTGTGTTCCATTGCAAGAGATGCGCTTGCATTAACCTCTT 1626
 QY 521 Ser 521
 DB 1627 TCT 1629

RESULT 3
 US-10-310-154-367
 ; Sequence 367, Application US/10310154
 ; Publication No. US20030233670A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Edgerton, Michael D
 ; APPLICANT: Chomet, Paul S.
 ; APPLICANT: Adams, Thomas H
 ; APPLICANT: Ruff, Thomas G.
 ; APPLICANT: Agarwal, Ameeta K.
 ; APPLICANT: Andrews, Jeffrey E.
 ; APPLICANT: Ball, James A.
 ; APPLICANT: Banu, G.
 ; APPLICANT: Bell, Erin
 ; APPLICANT: Boddupalli, Raghava
 ; APPLICANT: Deikman, Jill
 ; APPLICANT: Deng, Molian
 ; APPLICANT: Dong, Jintzhuo
 ; APPLICANT: Duff, Stephen M.
 ; APPLICANT: Galligan, Meghan M.
 ; APPLICANT: Hinchey, Brenda S.
 ; APPLICANT: Huang, Shihchieh
 ; APPLICANT: Johnson, G. Richard
 ; APPLICANT: Jung, Vincent
 ; APPLICANT: Kretzmer, Keith A.
 ; APPLICANT: Laccerelli, Lucille B.
 ; APPLICANT: Lai, Chao-Qiang
 ; APPLICANT: Lee, Gary
 ; APPLICANT: Lin, Jie-Yi
 ; APPLICANT: Liu, Jindong
 ; APPLICANT: Lu, Bin
 ; APPLICANT: Luedhy, Michael M.
 ; APPLICANT: Lund, Adrian
 ; APPLICANT: Madison, Linda L.
 ; APPLICANT: Malloy, Kathleen A.
 ; APPLICANT: McKiel, Christine L.
 ; APPLICANT: Miller, Philip W.
 ; APPLICANT: Padmavathi, Manthikanti
 ; APPLICANT: Parnell, Laurence D.
 ; APPLICANT: Start, William G.
 ; APPLICANT: Tennessee, Dan
 ; APPLICANT: Vidya, K. R.

```
; APPLICANT: Wang, Haiyun
; APPLICANT: Xun, Zhanguo
; APPLICANT: Xu, Nanfei
; APPLICANT: Yang, Chunzhi
; APPLICANT: Zeng, Xiaoping
; APPLICANT: Zhang, Qiang
; APPLICANT: Zhao, Ya'juan
; APPLICANT: Zhou, Li
; TITLE OF INVENTION: Gene Sequences and Uses Thereof in Plants
; FILE REFERENCE: 38-15(52796)B
; CURRENT APPLICATION NUMBER: US/10/310,154
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/337,358
; PRIOR FILING DATE: 2001-12-04
; NUMBER OF SEQ ID NOS: 736
; SEQ ID NO 367
; LENGTH: 1709
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (45)..(1607)
; OTHER INFORMATION:
; US-10-310-154-367

Alignment Scores:
Pred. No.: 0 Length: 1709
Score: 2256.00 Matches: 452
Percent Similarity: 86.76% Conservative: 0
Best Local Similarity: 86.76% Mismatches: 69
Query Match: 94.43% Indels: 0
Gaps: 0
DB: 6

US-09-857-581B-66 (1-521) x US-10-310-154-367 (1-1709)

QY 1 MetLeuLeuGluLeuAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeuArgPro 20
DB 45 ATGTGCTTGAACCTTCACCTGTTATGTGTTTGGCTCTGTTCTGCACCTTGCCTCC 104
QY 21 ThrPro***Ala***SerIysAlaLeuArgHisLeuProAsnProProSerPro***Pro 40
DB 105 ACACCCACGCAAAATCAAAAGACATTCGCCATCTCCCAACCCACCAAGCCCAAGCCT 164
QY 41 ArgLeuProPheIleGlyHis***HisLeuLeuAspIysLeuLeuHisTyrAla*** 60
DB 165 CGCTTCCTCCTTCAATAGACACCTTCATCTTAAAGACAACTTCTCCACTACGACATC 224
QY 61 IleAspLeuSerIysIysHisGlyProLeuPheSer*****PheGlySerMetProThr 80
DB 225 ATCGACCTCTCCAAAACATGGTCCCTTATCTCTCTACTTGTGGCTCATGCCAACCC 284
QY 81 ValValAlaSerThrProGluLeuPheIysLeuPheLeuGln*****GluAlaThrSer 100
DB 285 GTTGTGCTCCACACACAGAAATGTTCAAGCTCTTCTCCAAACGACAGGCAACTTCC 344
QY 101 Phe***ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp*****ValAla 120
DB 345 TTCAACAACAAGGTTCCAAACCTCAGCCATTAAGACGCTCACCTATGATAGCTCAGTGGCC 404
QY 121 *****Pro***GlyProTyrTyr***PheValArgIysLeuIleMetAsnAspLeu*** 140
DB 405 ATGGTTCCTCGGACCTTAAGTTCGTAAGATTCGTAGAGAGCTCATGAAACGACTTTC 464
QY 141 AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgIys***Leu 160
DB 465 AACGCACACACTGTAAACAAGTTGAGGCTTTGAGAGCCCAACAGATCCGCAAGTTCCT 524
QY 161 Arg***MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGluGluLeu 180
DB 525 AAGGTTATGGCCCAAGGCGCAGAGGCAACAGAGCCCTTGACCTTGACCGAGAGCTTCTG 584
QY 181 LysTyr***AsnSerThr***SerMetMet***LeuGlyGluAlaGluGluIleArgAsp 200
```

```
DB 585 AATGAGCAACAGACACCATCTCCATGATGATGCTCGCGCAGGCTGAGAGATCAAGAC 644
QY 201 IleAlaArgGluValLeuIysIle***GlyGlyTyrSerLeuThrAspPheIle***Pro 220
DB 645 ATCGCTCGGAGGTTCTTAAGATCTTTGGCGAATACAGCTCACTGACTTCACTCGGCCA 704
QY 221 LeuIys***LeuIysValGlyIysTyrGluIysAspIleAspAspIleLeuAsnIysPhe 240
DB 705 TTGAAGCATCTCAAGGTTGAAAGATATGAAAGAGATGAGACATCTTGAACAAGTTC 764
QY 241 AspProValValGluArgValIleIysIysArgArg***IleValArgArgArg***Asn 260
DB 765 GACCTGTGCTTGAAGGCTCATCAAGAGCCCGTGAGATGTGTAGAGGAGGAAGAAGAC 824
QY 261 GlyIu*****GluGlyGlu***SerGlyVal***LeuAspThrLeuLeuGluPheAla 280
DB 825 GGAAGGTTGTGAGAGGTGAGGTCAAGCGGGGTTTCTTGACACTTGTGTAATTCGCT 884
QY 281 GluAspGluThr***GluIleIysIleThrIys*****Ile***GlyLeuValAlaAsp 300
DB 885 GAGGATGAGACCATGAGATCAAAATCAACCAAGACATCAAGGCTTGTTCGCAC 944
QY 301 ***PheSerAlaGly***AspSerThrAla*****ThrGluTyrAlaLeuAlaGluLeu 320
DB 945 TTTTCTCGGACAGAACAGACTCCACAGCGGTGACACAGAGTGGGCAATTGGCAGAACTC 1004
QY 321 IleAsnAsnPro***ValLeu*****AlaArgIuGlu***TyrSerValAlaGlyIys 340
DB 1005 ATCAACAAATCCTAAGGTGTGGAAGAAAGGTCGTGAGAGGTTTACAGTGTGTGGAAAG 1064
QY 341 Asp***LeuValAspGluValAlaAspThrGlnAsnLeuProTyrIleArgAlaIleValIys 360
DB 1065 GACAGACTTGTGAGAGAGTGAACACTCAAAACCTTCCTTACATTAGAGCAATCGGAAG 1124
QY 361 GluThrPheArgMetHisProProLeuProValValIysArgIysCys***GluGluCys 380
DB 1125 GAGACATTCCTCGCATCACCCGCACTCCAGAGGTCAAAAGAAAGTGCACAAAGAGTGT 1184
QY 381 ***IleAsnGly***Val***ProGluGlyAlaLeu*****PheAsnValIleProGlnVal 400
DB 1185 GAGATTATGATATGATGATCCCAAGGAGGAGATGATTTCTTCAATGATAGCAAGTA 1244
QY 401 Gly***Asp***LysTyrTyrAspArgProSerGlu***ArgProGluArgPheLeuGlu 420
DB 1245 GGAAGAGACCCCAATACAGGACAGACCATCGAGTCCGCTCGAGAGGTTCTTACAG 1304
QY 421 Thr***AlaGluGlyGluAla*****LeuAspLeuArgGly***HisPheGlnLeuLeu 440
DB 1305 ACAGGGGCTGAAGGGGAAAGCAGGGCTCTTGATCTTAAGGGGCAACATTTTCAACTTCC 1364
QY 441 ProPheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***Ala 460
DB 1365 CCAATTTGGGTCTGGAGAGGAATGTGCCCTGAGATCAATCTGCTTACCTCGGAAATGGCA 1424
QY 461 ThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnIysGln 480
DB 1425 ACACTTCTTGACATCTTATTAAGTCTTCGACTTCGCAAGTCTGGGTCCACAAGAGACG 1484
QY 481 IleLeuIysGly***AspAlaIysValSerMetGluGluArgAlaGlyLeuThrValPro 500
DB 1485 ATATTGAAGGGGTGAGACGCCCAAGTTAGCAAGAGAGAGAGCCGGCTCTCATCTTCCA 1544
QY 501 ArgAlaHisSerLeuValCysValIleProLeuAlaGlyIleGlyValAlaSerIysLeuLeu 520
DB 1545 AAGGACATATGCTGTGTGTCTCCTCCTGCAAGATCGGGCTTGACATTAACCTCTT 1604
QY 521 Ser 521
DB 1605 TCT 1607

RESULT 4
US-10-732-923-309
; Sequence 309, Application US/10732923
```

```

; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15 (52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 309
; LENGTH: 1709
; TYPE: DNA
; ORGANISM: Glycine max
; US-10-732-923-309

Alignment Scores:
Pred. No.: 0 Length: 1709
Score: 2256.00 Matches: 452
Percent Similarity: 86.76% Conservative: 0
Best Local Similarity: 86.76% Mismatches: 69
Query Match: 94.43% Indels: 0
DB: Gaps: 0

US-09-857-581b-66 (1-521) x US-10-732-923-309 (1-1709)

QY 1 MetLeuLeuGluLeuAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeuArgPro 20
DB 45 ATGTTGCTTGAACCTGACCTGTTGTTATGTTGCTCTGTTCTGCACTTGCCTCC 104
QY 21 ThrPro***Ala***SerIysAlaLeuArgHisLeuProAsnProSerPro***Pro 40
DB 105 ACACCCACTGCAAAATCAAAAGCACTTGCCTATCTCCCAAAACCAAGCCAAAGCCT 164
QY 41 ArgLeuProPheIleGlyHis***HisLeuLeuLysAspLysLeuLeuHisIleValAla*** 60
DB 165 CGTCTCTCCCTTCATAGACACCTTCATCTTAAAGAACAAACTTCCCACTAGCAGCTC 224
QY 61 IleAspLeuSerLysLysHisGlyProLeuPheSer*****PheGlySerMetProThr 80
DB 225 ATCAACCTCTCCAAACAAACATGTCCTTATCTCTCTACTTATGCTTCATGCCAAC 284
QY 81 ValValAlaSerThrProGluLeuPheLysLeuPheLeuGln*****GluAlaThrSer 100
DB 285 GTTGTGCTCTCCACCAAGAACTTCTCAAGCTCTTCTCCAAAGCAAGGCAACTTCC 344
QY 101 Phe***ThrArgPheGlnThrSerAla***Arg***LeuThrIleAsp*****ValAla 120
DB 345 TTCAACACAAAGGTTCCAAACCTCAGCCATAAGACGCTCAGCTATGATAGCTCAGTGC 404
QY 121 *****Pro***GlyProTyrTyr***PheValArgLysLeuIleMetAsnAspLeu*** 140
DB 405 ATGTTGCTCTCCGACCTTACTGGAAGTTCTGAGGAAGCTCATCATGAAGACCTTCTC 464
QY 141 AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***Leu 160
DB 465 AACGCCACCACTGTAACCAACTTGAAGCTTTGAGAACCCCAAGATCCGCAAGTCTCT 524
QY 161 Arg***MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGluLeuLeu 180
DB 525 AGGTTATGCGCCAGAGCGCAGAGCAAGAGCCCTTGACTTGACCGAGAGACTTCTG 584
QY 181 LysThrPro***AsnSerThr***SerMetMet***LeuGlyGluAlaGluGluIleArgAsp 200
DB 585 AAATGACCAACAGACCATCTCCATGATGATGCTCGGAGAGCTGAGAGATCAGAGAC 644
QY 201 IleAlaArgGluValLeuLysIle***GlyGlyLysSerLeuThrAspPheIle***Pro 220
DB 645 ATCGTGGCGAGGTTCTTAAGATCTTGGCGAATACACCTCAGCTTCACTGCGGCA 704
QY 221 LeuLys***LeuLysValGlyLysTyrGlyLysAspGlyIleAspAspIleLeuAsnLysPhe 240
DB 705 TTGAAGCATCTCAAGTTGAGAAAGTATGAGAAAGAGATCGACGATCTTGAACAAAGTTC 764

```

```

QY 241 AspProValValGluArgValIleLysLysArgArg***IleValArgArgArg***Asn 260
DB 765 GACCTGTGCTGTAAGGCTCATCAAGAGCCCGTAGATGTTGAGGAGGAGAAAGAAC 824
QY 261 GlyGlu*****GluGlyGlyLys***SerGlyVal***LeuAspThrLeuLeuGluPheAla 280
DB 825 GAGAGAGTTGTTGAGGTTAGGTCAGCGGAGTTTCTTGAACCTTGGCTTGAATTCGCT 884
QY 281 GluAspGluThr***GluLysLysIleThrLys*****Ile***GlyLeuValValAsp 300
DB 885 GAGGATGAGACCATGAGATCAAAATCACCAAGAGCACATCAAGGCTCTTGTTCGAC 944
QY 301 ***PheSerAlaGly***AspSerThrAla*****ThrGluThrAlaLeuAlaGluLeu 320
DB 945 TTTTCTCGGACAGAACAGATCTCCAGCGGTGGCAACAGAGGAGCATTTGGAGAACTC 1004
QY 321 IleAsnAsnPro***ValLeu*****AlaArgGluGlu***TyrSerValValGlyLys 340
DB 1005 ATCAACAAATCTTAAGGTGTTGAAAAGGCTCGTAGAGAGGCTTACAGTGTGGGAAAG 1064
QY 341 Asp***LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLys 360
DB 1065 GACAGACTTGTGACAGCAAGTTGACACTCAAAACCTTCTTACATTAGAGCAATCGTAGAG 1124
QY 361 GluThrPheArgMetHisProProLeuProValValLysArgLysCys***GluGluCys 380
DB 1125 GAGACATTCGCGATGACCGCCGACCTCCAGTGTGTCAAAAGAGTGCACAGAGAGTGT 1184
QY 381 ***IleAsnGly***Ala***ProGluGlyAlaLeu*****PheAsnValTyrGlnVal 400
DB 1185 GAGATTAAATGATATGATATCCAGAGGAGGACATTAATCTTCAATGATATGCGAAGTA 1244
QY 401 Gly***Asp***LysTyrTyrAspArgProSerGlu***ArgProGluArgPheLeuGlu 420
DB 1245 GGAAGAGACCCCAAAATACAGGACAGACATCGAGTCCGCTCGTAGAGGTTCTTAAG 1304
QY 421 Thr***AlaGluGlyGluAla*****LeuAspLeuArgGly***HisPheGlnLeuLeu 440
DB 1305 ACAGGGGCTGAGAGGAGGAGGAGGCGCTTGAATGAGGAGCAAACTTTCAACTTCTC 1364
QY 441 ProPheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***Ala 460
DB 1365 CCAATTTGGCTGTGGAGAGAAATGTCCTGAGTCAATTTGCTACTTCCGGAATGCA 1424
QY 461 ThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGln 480
DB 1425 ACACTTCTTCATCTCTTATTCAGTGTCTGACTTGCAATGCTGGGTCCACAGAGACAG 1484
QY 481 IleLeuLysGly***AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValPro 500
DB 1485 ATATTGAAGGTGTGTAGCGCCAAAGTTAGCATGAGAGAGAGAGACCGGCTCAGCTGTCCA 1544
QY 501 ArgAlaHisSerLeuValCysValProLeuAlaArgIleGlyValAlaSerLysLeuLeu 520
DB 1545 AGGCAATATGATGTCTGTGTGTTCCACTTGCAAGAGATCGCGGTGATCTTAACCTCT 1604
QY 521 Ser 521
DB 1605 TCT 1607

```

```

RESULT 5
US-10-659-755-1
; Sequence 1, Application US/10659755
; Publication No. US2004012871A1
; GENERAL INFORMATION:
; APPLICANT: DIXON, RICHARD A.
; APPLICANT: LIU, CHANG-JUN
; APPLICANT: DEAYOORS, BETTINA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PRODUCTION OF FLAVONOID
; FILE REFERENCE: NLE: 007US
; CURRENT APPLICATION NUMBER: US/10/659,755

```

```

: CURRENT FILING DATE: 2003-09-10
: PRIOR APPLICATION NUMBER: 60/409,447
: PRIOR FILING DATE: 2002-09-10
: NUMBER OF SEQ ID NOS: 14
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 1
: LENGTH: 1824
: TYPE: DNA
: ORGANISM: Soybean
: US-10-659-755-1

```

Alignment Scores:

| | | | |
|------------------------|-----------|---------------|------|
| Pred. No.: | 9.65e-317 | Length: | 1824 |
| Score: | 2250.00 | Matches: | 451 |
| Percent Similarity: | 86.564 | Conservative: | 0 |
| Best Local Similarity: | 86.564 | Mismatches: | 70 |
| Query Match: | 94.188 | Indels: | 0 |
| DB: | 7 | Gaps: | 0 |

US-09-857-581B-66 (1-521) X US-10-659-755-1 (1-1824)

| | | |
|----|--|------|
| Oy | MetLeuLeuGluLeuLeuAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeuAlaArgPro | 20 |
| Db | ATGTGGCTTGAACCTGACCTTGTTATTGGTTTGGCTCTGTCTTCTGCACTTGGCTGCC | 1133 |
| Oy | ThrPro***Ala***SerIysAlaLeuArgHisLeuProAsnProProSerPro***Pro | 40 |
| Db | 114 ACACCACCTGCAAAATCAAAAGACACTTGGCATCTGCCAAACCCAGCAAGCCAAAGCCT | 173 |
| Oy | ArgLeuProPheHisIleGlyHis***HisLeuLeuIleAspIleValLeuHisIleTyrAla*** | 60 |
| Db | 174 CGCTTCCTCCCTCATAGAGACACTTCATCTCTTAAAAAGCAAACTTCTCACTAGACACTC | 233 |
| Oy | IleAspLeuSerIleYsHisIleGlyProLeuPheSer*****PheGlySerMetProThr | 80 |
| Db | 234 ATGACACTCTCCCAAAAAACATGATCCCTTATTTCTCTCTACTTTGGCTCCATGCAACC | 293 |
| Oy | ValValAlaSerThrProGluLeuPheIleValLeuGln*****GluAlaThrSer | 100 |
| Db | 294 GTTGTGGCTCCACACACAGAAATGTTCAAGCTCTTCTCCCAAGCAGAGCAAACTTCC | 353 |
| Oy | Phe***ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp*****ValAla | 120 |
| Db | 354 TTCAACACAAAGTTTCCAAACCTCAGCCATAAAGCCGCTCACTTAATGAAGCTCAATGACC | 4133 |
| Oy | *****Pro***GlyProTyrTrp***PheValArgIleValLeuIleMetAsnAspLeu*** | 140 |
| Db | 414 ATGCTTCCTCTCGACCTTATCTGGAAGTTCTGAGAGAGCTCATATATAGAAGACCTTCCC | 4737 |
| Oy | AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgIys***Leu | 160 |
| Db | 474 AACCCCAACCATGTAAACAAGTTGAGCGCTTTGAGAGACCCAAACACACCAGCTTCTT | 533 |
| Oy | Arg***MetAlaGln***AlaGluAla***IleProLeuAsp***ThrGluGluLeuLeu | 180 |
| Db | 534 AGGATTATGCGCCCAAGCGCAGAGCAGACAAAGCCCTTGAACCTTGACCGAGAGACTTCTG | 593 |
| Oy | LysTrp***AsnSerThr***SerMetMet***LeuGlyGluAlaGluGlnIleArgAsp | 200 |
| Db | 594 AAAAGGACCAACAGCACCATCTTCATGATGATGCTCGGCGAGCGAGAGAGATCAGAGAC | 653 |
| Oy | IleAlaArgGluValLeuIleIleIle***GlyGluTyrSerLeuThrAspPheIle***Pro | 220 |
| Db | 654 ATGCGCTGCGAAGGTTCTTAAGATCTTTGGCGAATACAGCTCACTGACTTCACTCGGCA | 7133 |
| Oy | LeuIys***LeuIysValGlyIleTyrGlyIleValArgIleAspAspIleLeuAsnIleAspHe | 240 |
| Db | 714 TTGAAGCATCTCAAGGTTGGAAGTATGGAAGAAGATGACGACATCTTGAACAAGTTC | 7737 |
| Oy | AspProValValGluArgValIleIleIleIleValArgIleArg***Asn | 260 |
| Db | 774 GACCTGTGCTTGAAGAGGTCATCAAGAGCGCGCTGAGATGTATGAGAGAGAAAGAAC | 8333 |

| | | | |
|--|------|---|------|
| QY | 261 | GLYGLU*****GIUGLYGLU***SerGIVal***LeuAspThrLeuLeuGluPheAla | 280 |
| Db | 834 | GGAGAGGGTGTGTGGAGGGGTGAGGTGACGGGGGTTTTCTTGACACTTGTGTTGAATTCGCT | 893 |
| QY | 281 | GLuAspGluThr***GluIleuYsIleThrIys****Ile***GlyLeuValValAsp | 300 |
| Db | 894 | GAGGATGAGACCATGAGATCAAAATCAACCAAGGACACATCGAGGGCTTGTGTGTGCAC | 953 |
| QY | 301 | ***PheSerIleagIy***AspSerThrAla*****ThrGluTrpAlaLeuAlaGluLeu | 320 |
| Db | 954 | TTTTTCTCGGAGGAGACAGACTCCACGCGGTGGCAACAAGTGGGATTTGGCAAACTC | 1013 |
| QY | 321 | IleAsnAsnPro***ValIleu*****AlaArgIuGluu**TySerValValGlyIys | 340 |
| Db | 1014 | ATCAACAATCTTAAGTGTCTTGAAAAAGGCTCTGTAGSAGGCTACAGATGTTGTGGAAAG | 1073 |
| QY | 341 | Asp***IleuValAspGluValAspThrGluAsnLeuProTyrIleArgAlaIleValIys | 360 |
| Db | 1074 | GACAGACTTGTGGACGAAGTTGACACTCAACCAAAACCTTCTTAACATTAAGCAATCGTAAAG | 1133 |
| QY | 361 | GluThrPheArgMetHisProProLeuProValValIysArgIysCys***GluGlyCys | 380 |
| Db | 1134 | GAGACATTCGCGCATCGACCCGCACTCCCACTGTTCAAAAGAAAGTGCACAGAAGATGT | 1193 |
| QY | 381 | **IleAsnGly***Val***ProGluGlyAlaLeu*****PheAsnValTTPGluVal | 400 |
| Db | 1194 | GAGATTAAATGATATGTGATCCACAGAGGAGCATTTGATCTTCAATGTATGGCAAGTA | 1253 |
| QY | 401 | GlyIy***Asp***IysTyrTrpAspArgProSerGluu***ArgProGluArgPheLeuGlu | 420 |
| Db | 1254 | GGAAGAGACCCCAAAATCTGGAGACAGACATCGAGTTCGGTCTTGAGAGGTTCTTGAG | 1313 |
| QY | 421 | Thr***AlaGluGlyGluAla*****LeuAspLeuArgGly***HisPheGluLeuLeu | 440 |
| Db | 1314 | ACAGGGCGGTGAAGGGAAGACGAGGCGCTTGATCTTAGGGGAACAATTTCAACTTCTC | 1373 |
| QY | 441 | ProPheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***Ala | 460 |
| Db | 1374 | CCATTGTGGTCTGGAGAGAGAAATGTGCTCGGAGTCAATCGGTACTCTGGGAATGGCA | 1433 |
| QY | 461 | ThrIleuLeuAlaSerIleuIleGlnCysPheAspLeuGluValIleuGlyProGlnGlyGln | 480 |
| Db | 1434 | ACACTTCTGTGATCTCTTATTCACTGCTTGCATCTTGAAAGTGGTGGGTCCACAAGACAG | 1493 |
| QY | 481 | IleIeuYsGly***AspAlaIysValSerMetGluGluArgAlaGlyLeuThrValPro | 500 |
| Db | 1494 | ATATTGAAGGTGTGTGACGCCAAAGTTAAGCATGAAAGAGAGAGCGGCGCTCACATGTTCCA | 1553 |
| QY | 501 | ArgAlaHisSerLeuValCysValProLeuAlaArgIleGlyValAlaSerIysLeuLeu | 520 |
| Db | 1554 | AGGGGACATGATCTTGTCTGTGTTCACATTCGAAGAGTCGGCGTTGCACTTAACCTCTT | 1613 |
| QY | 521 | Ser 521 | |
| Db | 1614 | TCT 1616 | |
| RESULT 6 | | | |
| US-10-505-145-3 | | | |
| ; Sequence 3, Application US/10505145 | | | |
| ; Publication No. US2005024101A1 | | | |
| ; GENERAL INFORMATION: | | | |
| ; APPLICANT: COLIVER, Steven Peter | | | |
| ; APPLICANT: DOBB, Roy Thomas | | | |
| ; APPLICANT: van der HILDEN, Hendrikus Theodorus Wilhelmus Maria | | | |
| ; TITLE OF INVENTION: PRODUCTION OF DADZEIN IN TRANSGENIC PLANTS | | | |
| ; FILE REFERENCE: 56159-5241 | | | |
| ; CURRENT APPLICATION NUMBER: US/10/505,145 | | | |
| ; PRIOR FILING DATE: 2004-08-20 | | | |
| ; PRIOR APPLICATION NUMBER: PCT/EP03/01465 | | | |
| ; PRIOR FILING DATE: 2003-02-13 | | | |
| ; PRIOR APPLICATION NUMBER: EP 02251404.6 | | | |
| ; PRIOR FILING DATE: 2002-02-28 | | | |
| ; NUMBER OF SEQ ID NOS: 59 | | | |

SOFTWARE: PatentIn version 3.2
 SEQ ID NO 3
 LENGTH: 1567
 TYPE: DNA
 ORGANISM: Glycine max
 US-10-505-145-3

Alignment Scores:

| Prod. No.: | 9_65e-317 | Length: | 1567 |
|------------------------|-----------|---------------|------|
| Score: | 2248.00 | Matches: | 450 |
| Percent Similarity: | 86.56% | Conservative: | 1 |
| Best Local Similarity: | 86.37% | Mismatches: | 70 |
| Query Match: | 94.10% | Indels: | 0 |
| DB: | 9 | Gaps: | 0 |

US-09-857-581b-66 (1-521) x US-10-505-145-3 (1-1567)

```

Qy      1 MetLeuLeuGluLeuAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeuAlaGPro 20
      |||::|||
Db      1 ATGGTGCTTGAACCTGACCTGGTTTATGGTTTGGCTCTGTTCTGACCTTGGCGTCC 60
Qy      21 ThrPro***Ala***SerLySaIaLeuAlaGHisLeuProAsnProProSerPro***Pro 40
      |||::|||
Db      61 ACACCCACTGCCAAATCAAAAGCACTTCCGCAATCTCCAAACCCCAAGCCCAAGCCCT 120
Qy      41 ArgLeuProPheIleGlyHis***HisLeuLeuAspLySLeuLeuHisTyAla*** 60
      |||::|||
Db      121 CGTCTTCCCTTCATGAGACCTTCATCTCTTAACAAACAACTTCCCTCACTGACATC 180
Qy      61 IleAspLeuSerLySHisGlyProLeuPheSer****PheGlySerMetProThr 80
      |||::|||
Db      181 ATGACACTCTCCAAAAAATGATGCTTATCTCTCTACTTGGCTCCATGCCAAC 240
Qy      81 ValValAlaSerThrProGluLeuPheLeuLeuGln****GluAlaThrSer 100
      |||::|||
Db      241 GTTGTGCTCTCCACACAGCAATGCTTCAAGCTCTTCTCCAAAGCAAGGCAACTTCC 300
Qy      101 Phe***ThrArgPheGlnThrSerAla***Arg***LeuThrTyraP****ValAla 120
      |||::|||
Db      301 TTCAACACAGGTTCCAAACCTCAGCCATAGACGCTCCTACCTTGTAGTCAGTGGCA 360
Qy      121 *****Pro***GlyProTyTrp***PheValArgLySLeuIleMetAsnAspLeu*** 140
      |||::|||
Db      361 ATGTGCTCCTCGGCGCCTACTGAGTGTGTGAGAGCTCATCATGAACGACTTCTC 420
Qy      141 AsnAlaThrThrValaLeu***LeuArgProLeuArgThrGlnGlnIleArgLyS***Leu 160
      |||::|||
Db      421 AACGCCACCACTGTAAACAGTTGAGGCTTTGAGGACCCCAACAGACGCGTAAAGTTCCTT 480
Qy      161 Arg***MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGluGluLeuLeu 180
      |||::|||
Db      481 AGGGTTATGGCCCAAGGCGCAGAGGACAGAAAGCCCTTGACTTGACCGAGGACTTCTG 540
Qy      181 LysTrp***AsnSerThr***SerMetMet***LeuGlyGluAlaGluGlnIleArgAsp 200
      |||::|||
Db      541 AAATGACCAACACACACATCTCATATGATGCTCGGCGAGGCTGAGGATCAGAGAC 600
Qy      201 IleAlaArgGluValLeuLeuIle***GlyGluTySerLeuThrAspPheIle***Pro 220
      |||::|||
Db      601 ATCCCTCGCAGAGTCTTAAGATCTTTGGCGAAATACACCTCCTCAGCTTATCTGCGCA 660
Qy      221 LeuLys***LeuLysValGlyLeuTyGlyLeuLysArgIleAspAspIleLeuAsnLysPhe 240
      |||::|||
Db      661 TTGAAGCACTTCAGGTTGAAAGATATAGAAAGAGATCGACGACATCTTGAACAAGTTC 720
Qy      241 AspProValValGluArgValIleLysLysArgArg***IleValArgArgArg***Asn 260
      |||::|||
Db      721 GACCTGTCGTTGAAGAGGTATCAAGAGCGCGTGAATCGTGAAGAGAGAGAAAGAAC 780
Qy      261 GlyGlu*****GluGlyGlu***SerGlyVal***LeuAspThrLeuLeuGluPheAla 280
      |||::|||
Db      781 GGAGAGGTTGTTGAGGTTGAGGTCAAGCGGGGTTTCTTGACACTTGTCTGAGTTCCGT 840
  
```

```

Qy      281 GluAspGluThr***GluIleLysIleThrLys*****Ile***GlyLeuValValAsp 300
      |||::|||
Db      841 GAGATGAGACTATGAGATCAAAATCACCAAGACACACATCAAGGCTTGTGTGAGC 900
Qy      301 ***PheSerAlaGly***AspSerThrAla*****ThrGluTrpAlaLeuAlaGluLeu 320
      |||::|||
Db      901 TTTTCTCGCAGAGAACAGACTCAACAGCGGTGGCAACAGATGGGCATTGGCAGAACATC 960
Qy      321 IleAsnAsnPro***ValLeu*****AlaArgGluGlu***TySerValValGlyLys 340
      |||::|||
Db      961 ATCAACAAATCTTAAGGTGTGAAAAAGCTCGTAGAGAGTCTACAGTGTGTGGAAAG 1020
Qy      341 Asp***LeuValAspGluValAspThrGlnAsnLeuProTyIleArgAlaIleValLys 360
      |||::|||
Db      1021 GACAGACTGTGACCAAGTTGACACTCAAAACCTTCTTACATTAGACCAATCGTGAAG 1080
Qy      361 GluThrPheArgMetHisProProLeuProValValLysArgLysCys***GluGluCys 380
      |||::|||
Db      1081 GAGACATTCCGATGACACCCGCACTCCAGTGTCAAAAGAAAGTGCACAGAAAGGTGT 1140
Qy      381 ***IleAsnGly***Val***ProGluGlyAlaLeu*****PheAsnValTrpGlnVal 400
      |||::|||
Db      1141 GAGATTATGGAATATGATATCCAGAGGAGCATTTCTTCTCATGATATGCAAGTA 1200
Qy      401 Gly***Asp***LysTyTrpAspArgProSerGlu***ArgProGluArgPheLeuGlu 420
      |||::|||
Db      1201 GGAAAGAGACCCCAAAATCTGGAGCAGACACATCGAATTCGCTCTAGAGGTTCTAGAG 1260
Qy      421 Thr***AlaGluGlyGluAla*****LeuAspLeuArgGly***HisPheGlnLeuLeu 440
      |||::|||
Db      1261 ACAGGGGCTGAAAGGAGAGAGAGAGGAGGCTCTTGAATCTTAGGGAACAATTTCAACTTCTC 1320
Qy      441 ProPheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***Ala 460
      |||::|||
Db      1321 CCAATTGGGTCTGGAGAGAAATGTGCTCCGAGTCAATCTGCTACTTCCGGAATGCGCA 1380
Qy      461 ThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGln 480
      |||::|||
Db      1381 ACACCTTCTGACATCTCTTATTCAGTCTGCTGACCTTCGACCTTCGACCTTCGACCTTCG 1440
Qy      481 IleLeuLysGly***AspAlaLysValSerMetGlyGluArgAlaGlyLeuThrValPro 500
      |||::|||
Db      1441 ATATTGAAGGCTGTGACCGCAAAAGTTAGATGAGAAAGAGAGACCGGCTCAGCTTCCA 1500
Qy      501 ArgAlaHisSerLeuValCysValProLeuAlaArgIleGlyValAlaSerLySLeuLeu 520
      |||::|||
Db      1501 AGGGCAATATGCTTGTGCTGTGTTCCACTTGCAAGGATCGGCGTGCATCTAAATCTCCTT 1560
Qy      521 Ser 521
      |||
Db      1561 TCT 1563
  
```

RESULT 7
 US-10-739-930-3497
 ; Sequence 3497, Application US/10739930
 ; Publication No. US20040216190A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kovalic, David K.
 ; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
 ; FILE REFERENCE: 38-21(53577)B
 ; CURRENT FILING DATE: 2003-12-18
 ; NUMBER OF SEQ ID NOS: 11088
 ; SEQ ID NO 3497
 ; LENGTH: 1974
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: GLYMA-23APR03-CLUSTER333_17
 US-10-739-930-3497

Alignment Scores:

| | | | |
|------------------------|-----------|---------------|------|
| Pred. No.: | 2.04e-299 | Length: | 1974 |
| Score: | 2130.00 | Matches: | 430 |
| Percent Similarity: | 83.11% | Conservative: | 3 |
| Best Local Similarity: | 82.53% | Mismatches: | 78 |
| Query Match: | 89.16% | Indels: | 10 |
| DB: | 8 | Gaps: | 1 |

US-09-857-581B-66 (1-521) X US-10-739-930-3497 (1-1974)

| | | | |
|----|--|--|------|
| OY | | MethLeuLeuGIuLeuAlaLeuGIuLeu***ValLeuAlaLeuPhe***HisLeuAspPro | 20 |
| Dd | | ANtTGCTCGAACTTCGACCTGGTGTGTGTGTGTAGCTTGGATTCTGCACCTGGATGCC | 318 |
| OY | | ThrPro**Ala***SerLySAlaLeuArRghisLeuProAanProProSerPro**Pro | 40 |
| Dd | | ACACCAGACTGAATCAAAAGACAATTGGCCACCTCCCAAACCTCCCAAGGCCAAAGCCT | 378 |
| OY | | ArgLeuProPheIleGLYHis***HisLeuLeuLYsAspLYsLeuLeuHisTYrAla*** | 60 |
| Dd | | CGTCTCCCTTCATTTGGGACACCTTCACCTTTAAAAGAATAAACCTTCTCACATATGACCTC | 438 |
| OY | | IleAspLeuSerLySLeuHisGLYProLeuPheSer*****PheGLYSerMetProThr | 80 |
| Dd | | ATCGATCTCTCCAAAAAGCATGGCCCCCTTAATCTCTCTCTCTCTGGATACGGCAACC | 498 |
| OY | | ValValAlaSerThrProGLuLeuPheLYsLeuPheLeuGIN****GlulAlaThrSer | 100 |
| Dd | | GTCGGGGGGCTCCACCCCTGAGTGTTCAAAGCTCTTCTCCCAACCACGAGGAAGCTTCC | 558 |
| OY | | Phe***ThraGPheGLInThSerAla***Arg***LeuThryTYrAsp*****ValAla | 120 |
| Dd | | TTCACAACAAGGTTCCAACCTCTGCCTTAAGACCCCTCACTTACGACAACTCTGTGGCC | 618 |
| OY | | ****Pro****GLYProTYrTrp***PheValaGLYSLeuIleMetAsnAspLeu*** | 140 |
| Dd | | ATGTTTCATTTGGACCTTACTCGAAGTTCGAGAGAACTCATATATAAGACCTTCTTC | 678 |
| OY | | AsnAlaThrThrValaasn***LeuarRPProLeuaRGThngInGlnIleArgLYs***Leu | 160 |
| Dd | | AACGCCACACCGACGACACAGCTCAGGCTTTGAGACCCCAACAGATCCGCAAGTCTCT | 738 |
| OY | | Arg***MetAlaGLIn***AlaGLuAla***LYsProLeuasp***ThrGLuGLuLeuLeu | 180 |
| Dd | | AGGGTTATAGCCCAAGCGACAGAGCCCAAGGCCCTTGAACGTACACGAGAGGCTTCTC | 798 |
| OY | | LysTRP***AanSerThr***SerMetMet***LeuGLYGLuAlaGLuIleArgAsp | 200 |
| Dd | | AAATGACCAACACAGACCATCTCCACATGATGATCTCGCGAGGCTCGAATGATATCGAACC | 858 |
| OY | | IleAlaARGGLuValLeuLYsIle***GLYGLUTyrSerLeuThrAspPheIle***Pro | 220 |
| Dd | | ATCGTCCCGAGGTTCTTAGATCTTTCGGCGAAATACACCTCACATCTTCATCTGGGCT | 918 |
| OY | | LeuLYs***LeuLYsValaGLYLYsTYrGLuLYsArgIleAspAspIleLeuAsnLYsPhe | 240 |
| Dd | | TTGAAGTATCTCAAGGTTGAAAGATATGAAAGAGATGATGATCATCTTGAACAAGTTC | 978 |
| OY | | AspProVALaGLuArgValIleLeuLYsArgAg***IleValArgArgArg***asn | 260 |
| Dd | | GACCTGTGCTGTTGAAAGGGTCACTCAAGAGCCCGCTGAGATCGTTCAGAGAGAGAAAGAAC | 1038 |
| OY | | GLYGLu*****GLuGLYGLu***SerGLYVal***LeuAspThrLeuLeuGLuPheAla | 280 |
| Dd | | GGAGAAAGTGTGAGAGCGGACGCGGCTTCTCTCGACACTTGTGCTGAATTCGCT | 1098 |
| OY | | GLuAspGLuThr***GLuIleLYsIleThrLYs*****Ile***GLYLeuValValAsp | 300 |
| Dd | | GAGGACGAGACCATGAGATCAAAATTCACAAAGAGACAAATCAAGGCGCTTGTGTGCAC | 1158 |
| OY | | PheserAlaGLY***AspserThrAla*****ThrglUTPrAlaLeuAlaGLuLeu | 320 |
| Dd | | TTTTTCTCTGAGGAGACAGATTTCACAGCGGTGGCAACAGATGGCAATTGGCAAGCTTC | 1218 |

| | | | |
|--|------|--|------|
| QY | 321 | lleasnbnpr***Valleu*****Alarngluolu***TyrserValValglylys | 340 |
| | 1219 | GTGGAGAGGCTTCA-----GCTGTGGGGCAAA | 1248 |
| QY | 341 | Asp***LeuValAaSPgluValAspThrGlnAsnLeuProTyrIleacAlaIleVallys | 360 |
| Db | 1249 | GATAGACTCGTGAAGAGTTGACACTCAAAACCTTCTTACATTAGGGCATTGTGAAG | 1308 |
| QY | 361 | GlutThrPheargMetHisProProLeuProValIalysarglyscys***GluGluCys | 380 |
| Db | 1309 | GAGACATTCGAAATGCACCACCTCCAGTGTGTCAAAAGAAAGTCAACAGAAAGATGT | 1368 |
| QY | 381 | ***lleasnngly***Val***ProGluGlyAlaIleu*****PheAsnValITrpgIuVal | 400 |
| Db | 1369 | GAGATTAAATGGGATGTGATCCCGAGAGGAGCATGTGTTCTTTCAATGTTGGCAAGTA | 1428 |
| QY | 401 | Gly***Asp***LysTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGlu | 420 |
| Db | 1429 | GGAAAGGACCCCAATATCTGGGAGACAGCATCAGAAATTCCGTCCCGAAGGTTCTTGAA | 1488 |
| QY | 421 | Thr***AlaGluGlyGluAla*****LeuaspLeuarggly***HisPheGlnLeuLeu | 440 |
| Db | 1489 | ACTGGTGTGTAAGGGGAGGAGCGGCGCTTGATCTTGAGGGGCGACGATTTCCACTCTTC | 1548 |
| QY | 441 | ProPheGlySerGlyArg***MetCysProGlyVal***IeuAlaTrpSerGly***Ala | 460 |
| Db | 1549 | CCATTTGGTGCTGGAGAGAGATGTGCCCTGGCCTCAATTTGGCTACTTCAGGAATGCA | 1608 |
| QY | 461 | ThrIeuLeuAlaSerLeuIleGlnCysPheaspLeuGlnValIleuGlyProGlnGlyGln | 480 |
| Db | 1609 | ACACTTCTGTGATCTCTTATTCATTCGTTGACCTGCAAGTCTGGGCGCTTCMAAGCA | 1668 |
| QY | 481 | IleLeuArgly***AspAlaAlaValSerMetGluGluArgAlaGlyLeuThrValPro | 500 |
| Db | 1669 | ATATTGAAAGGTGATGATCCCAAGATTAGCATGGAAGAGAGAGCTGGCGCTTCA | 1728 |
| QY | 501 | ArgAlaHisSerLeuValCysValProIeuAlaArgIleGlyValAlaIaSerLyLeuLeu | 520 |
| Db | 1729 | AGGGACACTAGTCTCGATTGTGTTCACCTTGCAAGAGATCGCGCTTGATCTAACTCCTT | 1788 |
| QY | 521 | Ser 521 | |
| Db | 1789 | TCT 1791 | |
| RESULT 8 | | | |
| US-10-411-115-3 | | | |
| Sequence 3, Application US/10411115 | | | |
| Publication No. US20040003431A1 | | | |
| GENERAL INFORMATION: | | | |
| APPLICANT: Mizutani, Masako | | | |
| APPLICANT: Kasumi, Takaaki | | | |
| APPLICANT: Ayabe, Shin-ichi | | | |
| APPLICANT: Akashi, Tomoyoshi | | | |
| TITLE OF INVENTION: Genes Coding for Flavone Synthases | | | |
| FILE REFERENCE: 001560-383 | | | |
| CURRENT APPLICATION NUMBER: US/10/411.115 | | | |
| PRIOR FILING DATE: 2003-04-11 | | | |
| PRIOR APPLICATION NUMBER: US/09/672,785 | | | |
| PRIOR FILING DATE: 2000-09-29 | | | |
| PRIOR APPLICATION NUMBER: PCT/JP00/04379 | | | |
| PRIOR FILING DATE: 2000-01-30 | | | |
| PRIOR APPLICATION NUMBER: PCT/JP00/00490 | | | |
| PRIOR FILING DATE: 1999-01-28 | | | |
| PRIOR APPLICATION NUMBER: JP 11-205229 | | | |
| PRIOR FILING DATE: 1999-01-19 | | | |
| PRIOR APPLICATION NUMBER: JP 11-22427 | | | |
| PRIOR FILING DATE: 1999-01-29 | | | |
| NUMBER OF SEQ ID NOS: 8 | | | |
| SOFTWARE: PatentIn version 3.0 | | | |
| SBO ID NO 3 | | | |
| LENGTH: 1730 | | | |
| TYPE: DNA | | | |
| ORGANISM: Toxentia hybrida | | | |


```

; TYPE: DNA
; ORGANISM: Torenia hybrida
; FEATURES:
; OTHER INFORMATION: Nucleotide sequence encoding a protein having an
; OTHER INFORMATION: activity to directly convert Flavanone to Flavone
US-10-411-225-3

```

Alignment Scores:

| Pred. No.: | 2,3e-126 | Length: | 1730 |
|------------------------|----------|---------------|------|
| Score: | 944.50 | Matches: | 198 |
| Percent Similarity: | 57.56% | Conservative: | 95 |
| Best Local Similarity: | 38.90% | Mismatches: | 189 |
| Query Match: | 39.54% | Indels: | 28 |
| DB: | 8 | Gaps: | 8 |

US-09-857-581b-66 (1-521) x US-10-411-225-3 (1-1730)

```

QY 20 ProThrPro**Ala**SerIysAlaLeuArgHisLeuProAsnProSerPro** 39
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 103 CCAACCACTTCTCTCTCTCTCTCGCGCA-AGGGACCAACGTCCTCGCGCTCTC 161
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 40 ProArgLeuProPheIleGlyHis**HisLeuLeuLysAspLysLeuLeuHisIleYrAla 59
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 162 ---TCCCTACCAATATGGCCACCTCCACCTCTCGGCCCAAGA---CTCCACCAACAG 215
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 60 **IleAspLeuSerLysHisIleGlyProLeuPheSer*****PheGlySerMetPro 79
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 216 TTCCTAGAAATTCCTCACTCAATATACGCCCTTATGATCCAGCTCAAGCTCGATCCCG 275
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 80 ThrValAlaIleSerThrProGluLeuPheLysLeuPheLeuGln*****GluAlaIthr 99
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 276 TGGGTCGTGGCTCGACGCCCGAGCTCGAGAGAGATTCTTAAAGCAACAG---CTC 332
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 100 SerPhe**ThrArgPheGlnIthrSerAla***Arg***LeuThrIYrAsp*****Val 119
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 333 GCGTCTCTCCCTCGCAAGCACTCTACGCCATAGACATCGTCACTACGACTCGCTCTT 392
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 120 Ala*****Pro**GlyProIYrTrp***PheValArgLysLeuIleMetAsnAspLeu 139
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 393 GCTTTCTCTCCGTAAGAGACCTTACTGAGTACTCAAGAACTGTGTACTTACCTACAGACTG 452
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 140 **AsnAlaIthrThrValaIen***LeuArgProLeuArgThrGlnGlnIleArgLys** 159
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 453 CTCGAGCGGAGAACTCGAGACTTTCAGGCCATTATGAAATCTCGAGCTGAGTCTCTT 512
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 160 LeuArg**MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGluGluLeu 179
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 513 CTCGACGTTCTGTATGACAAAGAGCTTTAAGGCGAGAGTGTGAATGTGACAGACAGACTG 572
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 180 LeuLysTrp**AsnSerThr***SerMetMet***Leu----- 192
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 573 GTTAGGCTGACGAGCAATGTGATATCCCACTGATGCTGAGCTAAGTCTCGGAAGAT 632
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 193 ---GlyGluAlaGluGluIleArgAspIleAlaArgGluValLeuLysIle**GlyGlu 211
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 633 GAAGGCGATCTGAGGCGGAGAAAGATATCGCAGAGTACGCGAGATATTTGGGGA 692
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 212 TyrSerLeuThrAspPheIle***ProLeuLys***LeuLysValGlyLysIYrGluLys 231
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 693 TTCGATGTTACGAGCAATATATGTTTTCAGAAATTCATCTGCGAGGAGTAAGAACAG 752
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 232 ArgIleAspAspIleLeuAsnLysPheAspProValAlaGluIthrValIleLysIYrArg 251
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 753 AGGTCAAGGATATTCAGAGAGGTATGATGCTTGTGCTGAGAAATATATAGTATAGA 812
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 252 Arg**IleValArgArgArg**AsnGlyGlu***GluGly-----Glu** 268
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 813 GAGAGA-----TCGAGAGAGCAAAATCGGATAGAGATGTGCGGTAAATAGAGAG 866
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 269 SerGlyVal**LeuAspIthrLeuLeuGluPheAlaGluAspGluIthr***GluIleLys 288
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 867 GCCAAGGATTTTCTTGTATGTTGCTTGTATGATGTGATGAGAGTGGGAGACGAGGTCAAA 926
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

QY 289 IleThrLys*****Ile***GlyLeuValValAsp***PheSerAlaGly**AspSer 308
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 927 TTCCTAGAGAGCATCTCAAGGCTTGTGATTCGTGATTTCTTACGCCGCGGTACGACACA 986
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 309 ThrAla*****ThrGluTrpAlaLeuAlaGluLeuIleAsnAsnPro**ValLeu*** 328
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 987 ACAGCCATAGCACCAAGTGGGCGCATCGCGAGCTCATCAACACCCGAAACGCTTGAAG 1046
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 329 **AlaArgGluGlu**TyrSerValValGlyLysAsp***LeuValAspGluValAsp 348
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1047 AAGCCCAAGAAATATATCCGAGATCATCGAACCAGCGGATGTCTACAGATCCGAC 1106
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 349 ThrGlnAsnLeuProTyrIleArgAlaIleValLysGluThrPheArgMetHisProPro 368
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1107 GCCCCAGACCTTACCTTACTCCAGGCCATCATCAAGAGACGTTCGGGTCCACCCACCG 1166
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 369 LeuProValValLysArgLysCys**GluGluCys**IleAsnGly**Val***Pro 388
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1167 ATCCCGATGCTCTCGGTAAAGTCCACCTCCGATTCGACCGGTCAACCGCTAACAAATCCAA 1226
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 389 GluGlyAlaLeu*****PheAsnValTrpGlnValGly**Asp**LysIYrTrpAsp 408
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1227 GCCAAGAGCTCTTGTTCGTGAACATATGTCATCGATGTCGAAACCTTAATTACTGGAA 1286
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 409 ArgProSerGlu**ArgProGluArgPheLeuGluIthr**AlaGluGlyGluAla*** 428
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1287 AGCCCTATGAGATTCAGGCGCCGAGCGGTCTTGGAGAAAGGACGCGAG----- 1334
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 429 **LeuAspLeuArgGly**HisPheGlnLeuLeuProPheGlySerGlyArg**Met 448
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1335 TCCATGACGATCAAGGCGCCAGCATTTGAGCTTCTGCTTTGGAGCGGCGCGAGGCGC 1394
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 449 CysProGlyVal**LeuAlaIthrSerGly***AlaThrLeuLeuAlaSerLeuIleGln 468
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1395 TGTCGGGATGTGCTGCGCTATPACAGAGGTGTGATGATCTTGGAGCATGTTCCAG 1454
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 469 CysPheAspLeuGlnValLeuGlyProGlnGlyGlnIleLeuLysGly**AspAlaLys 488
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1455 TGCTTTCGAC-----TGGAAATTCGACATGTTCCGGCAATAT 1493
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 489 ValSerMetGluGluArgAlaGlyLeuIthrValProArgAlaHisSerLeuValCysVal 508
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1494 GTGCACATGACCGAAGCGTGTGATTCGATTCGAGCGCTCCGAGAGCGTTCATGTGTTCCCG 1553
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 509 ProLeuAlaArgIleGlyValAlaIleSer 517
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1554 TTGTATTCACGGGTTGACCCGGCCACA 1580
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

RESULT 10

```

US-10-411-115-1
; Sequence 1, Application US/10411115
; Publication No. US20040003431A1
; GENERAL INFORMATION:
; APPLICANT: Mizutani, Masako
; APPLICANT: Kasumi, Takaki
; APPLICANT: Ayabe, Shin-ichi
; APPLICANT: Akashi, Tomoyoshi
; TITLE OF INVENTION: Genes Coding for Flavone Synthases
; FILE REFERENCES: 001560-383
; CURRENT APPLICATION NUMBER: US/10/411,115
; PRIOR APPLICATION NUMBER: US/09/672,785
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JP00/04379
; PRIOR FILING DATE: 2000-01-30
; PRIOR APPLICATION NUMBER: PCT/JP00/00490
; PRIOR FILING DATE: 1999-01-28
; PRIOR APPLICATION NUMBER: JP 11-205229
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: JP 11-22427
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0

```

```

; SEQ ID NO 1
; LENGTH: 1724
; TYPE: DNA
; ORGANISM: Antirrhinum majus
; FEATURE:
; OTHER INFORMATION: Nucleotide sequence encoding a protein having an
; OTHER INFORMATION: activity to directly convert flavanone to flavone
US-10-411-115-1

Alignment Scores:
Pred. No.: 3, 2e-126 Length: 1724
Score: 943.50 Matches: 198
Percent Similarity: 57.314 Conservative: 88
Best Local Similarity: 39.684 Mismatches: 179
Query Match: 39, 498 Indels: 34
DB: Gaps: 9

US-09-857-581b-66 (1-521) x US-10-411-115-1 (1-1724)

QY 33 ProAsnProProSerPro***Pro-Arg-----Leupr 43
DB 87 CCGACCCCTCTTAACCGGACCGCGCAAGACCCCGCGGCCCATTAAGCCCTCC 146
QY 43 oPheIIeGIYHIS***HisLeuLeuYsAePLysLeuLeuHISYrAla***IleAspLe 63
DB 147 CTTAATAGGCCACTTACACTCTCTCGGCCAAG---CTCCACACACCTTCCACCAATT 203
QY 63 uSerLYsLYsHISGLYProLeuPheSer*****PheGLYSerMetProThrValValAl 83
DB 204 CTCGCAACGCTACGGCCGCTCATCCAGCTCTACCTCGGCTCCGCTCCAGCGCTCGCG 263
QY 83 aSerThrProGLuLeuPheLYsLeuPheLugIn*****GluAlaThrSerPhe***Th 103
DB 264 TTCACGCGCCGAACTGCGCCGCAATTCCTCAAGACCGCACGA---CTGACTTCTGTC 320
QY 103 rArgPheGLnThrSerAla***Arg***LeuThrTYrAsp*****ValAla*****Pr 123
DB 321 CCGCAAGACTCCACCGCCCATCGACATCGTCAGTACGCTCGTGGCTTGGCGGCC 380
QY 123 o**GlyProTYrTrp***PheValArgLYsLeuIleMetAsnAspLeu***AsnAlaTh 143
DB 381 GTACGGGCGGTACTGGAATTCATCAAGAAATTATGTACTTACGACTGCGGTGCCG 440
QY 143 rThrValAsn***LeuArgProLeuArgThrGLnGLnIleArgLYs***LeuArg***Me 163
DB 441 GAACTTAGGCCATTTCAGCCCATTAAGAGCTTTGGAGGCAACAGTTTCTTGAGAAATT 500
QY 163 tAlaGLn***AlaGLuAla***LYsProLeuAsp***ThGLuGLuLeuLeuLYrTrp** 183
DB 501 GTACGAGAAAACAGACGAAACAGAGCTTTAATGTACAGAGAGCTTGGAAGCTGAC 560
QY 183 *AsnSerThr***SerMetMet***Leu-----GlyGLuAl 195
DB 561 GAGTAATGTGATCATGAATGATGTGGGATCAGGTGTTGGGGAGCGAAGGGGAGGC 620
QY 195 aGLuGLuIleArgAspIleAlaArgGLuValLeuLYrIle***GLYGLuTYrSerLeuTh 215
DB 621 GGAAGTGGCGGAGCGGTGATAGCGAGGTGACCGAGATTTTGGAGTTTGATGTGTC 680
QY 215 rAspPheIle***ProLeuLYs***LeuLYsValGLYrTYrGLuLYsArgIleAspAs 235
DB 681 GGAAGATTGTTGCTTTGTAAAGATTGGATCTCCAGGCGATTGGAAGAGGTGCGAGA 740
QY 235 pIleLeuAsnLYsPheAspProValValGLuArgValIleLYsLYsArgIleAspAs 255
DB 741 TATTAGGAGGAGGTATGCTTTGTTGAGAAAGATTATTGTGATAGGAGAGCTTG- 798
QY 255 lArgArgArg***AsnGLYGLuLYs***GLuGLYGLuLYs***SerGLYVal***LeuAspTh 275
DB 799 -AGGTTGAGGGGGGTGTGTGTGAGAGGGGTGCGAGAGGTGAAGAT---TTTTGGATAT 854
QY 275 rLeuLeuGLuPheAlaGLuAspGLuThr***GLuIleLYsIleThrLYs*****Ile** 295

```

```

DB 855 GTTGTGATGTCGATGAGAGTGAAGAAATCGAGGTGAGTTTACAGGAGCATCTCA 914
QY 295 *GlyLeuValValAsp***PheSerAlaGLY***AspSerThrAla*****ThGLuTYr 315
DB 915 AGCTTTGATTCGTGATTTCTTCACTGCGGTACAGACACACAGCAATTCACAAAGAA 974
QY 315 pAlaLeuAlaGLuLeuIleAsnAsnPro***ValLeu*****AlaArgGLuGLu***Ty 335
DB 975 GCGAATGAGGAGAACTTATGCAATTCCAATTTACTCAAAAAGGCTCAAGAAAGATGCA 1034
QY 335 rSerValValGLYLYsAsp***LeuValAspGLuValAspThrGLnAsnLeuProTYrI 355
DB 1035 CAAGCTCAGGATGATCACAAGGTTGTGACAGAAATCCAGCGCCCTAATCTTACT 1094
QY 355 eArgAlaIleValLYsGLuThrPheArgMetHisProProLeuProValValLYsArgLY 375
DB 1095 CAACGAGATCAATAAAGAAACGTTCCGTCTCACCTCCATCCCATCTCACTAGAAA 1154
QY 375 rCYs***GLuGLuCYs***IleAsnGLY***Val***ProGLuGLuAlaLeu*****Ph 395
DB 1155 ATCAATTTCTGACGTTGTGTCACGCGGTACAGATCCGTCMAAACGCTATTGTTGT 1214
QY 395 eLeuValTYrGLnValGLY***Asp***LYsTYrTPAspArgProSerGLY***ArgPr 415
DB 1215 CAACCTTGTCATCGAGGAAAGATCTTAACCTAGGAAATCCAGATGAGTTCCGACC 1274
QY 415 oGLuArgPheLeuGLuThr***AlaGLuGLuGLuAla*****LeuAspLeuArgLY** 435
DB 1275 CAGAGGTTTCTCGAAGAAAGGG-----ACGGGATCGATGAGCTTAAAGGCGCA 1322
QY 435 *HisPheGLnLeuLeuProPheGLYSerGLYArg***MetCYsProGLYValI***LeuAl 455
DB 1323 GCATTTGCAAGTTGCTCCGCTTGGCAAGCGGCGGCGGCGGCTGCCGGGATGTTTGA 1382
QY 455 aThrSerGLY***AlaThrLeuLeuAlaSerLeuIleGLnCYsPheAspLeuGLuVal 475
DB 1383 CATGACGAGGTTGTTAGTAATTTCGGGCTATGTCAGTGTGATTGGAATCTG--- 1440
QY 475 uGLYProGLnGLYGLnIleLeuLYsGLY***AspAlaLYsValSerMetGLuGLuArgAl 495
DB 1441 ----CCCGATGTGTG-----AMGTGCGTGCATGATGCCAGGCGGCC 1478
QY 495 aGLYLeuThrValProArgAlaHisSerLeuValCYsValProLeuAlaArgIle 513
DB 1479 CGGTTGACGCGCTCCACGTCGCAATGATTTGTTGTCATTTGTCACAGGAT 1533

RESULT 11
US-10-411-225-1
; Sequence 1, Application US/10411225
; Publication No. US20040261146A1
; GENERAL INFORMATION:
; APPLICANT: Mizutani, Masako
; APPLICANT: Kasumi, Takaaki
; APPLICANT: Ayabe, Shin-ichi
; APPLICANT: Akashi, Tomoyoshi
; TITLE OF INVENTION: Genes Coding for Flavone Synthases
; FILE REFERENCE: 001560-383
; CURRENT APPLICATION NUMBER: US/10/411,225
; PRIOR APPLICATION NUMBER: US/09/672,785
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JP00/04379
; PRIOR FILING DATE: 2000-01-30
; PRIOR APPLICATION NUMBER: PCT/JP00/00490
; PRIOR FILING DATE: 1999-01-28
; PRIOR APPLICATION NUMBER: JP 11-205229
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: JP 11-22427
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1724

```

```

; TYPE: DNA
; ORGANISM: Antirrhinum majus
; FEATURE:
; OTHER INFORMATION: Nucleotide sequence encoding a protein having an
; OTHER INFORMATION: activity to directly convert flavanone to flavone
US-10-411-225-1

```

Alignment Scores:

| | | | |
|------------------------|----------|---------------|------|
| Pred. No.: | 3 2e-126 | Length: | 1724 |
| Score: | 943.50 | Matches: | 198 |
| Percent Similarity: | 57.314 | Conservative: | 88 |
| Best Local Similarity: | 39.684 | Mismatches: | 179 |
| Query Match: | 39.498 | Indels: | 34 |
| DB: | 8 | Gaps: | 9 |

US-09-857-581B-66 (1-521) x US-10-411-225-1 (1-1724)

[illegible][illegible]

```

; FEATURE: Nucleotide sequence encoding a protein having an
; OTHER INFORMATION: activity to directly convert flavanone to flavone
; OTHER INFORMATION: activity to directly convert flavanone to flavone
US-10-411-115-7

```

Alignment Scores:

| | | | |
|------------------------|--------|---------------|-----|
| Pred. No.: | 177 | length: | 190 |
| Score: | 521.50 | Matches: | 190 |
| Percent Similarity: | 57.46% | Conservative: | 91 |
| Best Local Similarity: | 38.85% | Mismatches: | 183 |
| Query Match: | 38.57% | Indels: | 25 |
| DB: | 6 | Gaps: | 8 |

US-09-857-581B-66 (1-521) x US-10-411-115-7 (1-1770)

[illegible]

| | | | |
|----|------|---|------|
| Db | 924 | GGACCCGACACGACGCGGATCGTGTGTGAATGGCCGATAGCAAGATCAACATCCGA | 983 |
| OY | 325 | ***ValLeu*****AlaArgGluGlu***TyrSerValValGlyLysAsp***LeuVal | 344 |
| Db | 984 | AATGTGTGTAAGAAAGCTCAAGAGATTTGCCAACAATCGTCGGATTCCAGCAATTCG | 1043 |
| OY | 345 | AspGluValAspThrGlnAsnLeuProGlyTlleArgAlaIleValLysGluThrPheArg | 364 |
| Db | 1044 | CAAAATATCCGACGCCCCCAATCTGCCCCCTTACCTTCAGCCCTCATCAAGAAACATTCCG | 1103 |
| OY | 365 | MetHisProProLeuProValValLysArgLysCys**GluGluCys**IleAsnGly | 384 |
| Db | 1104 | CTCACACCTCCAAATCCCAATCTGGACGAGAAATCGATTCCGACTCGTCATCGACGCG | 1163 |
| OY | 385 | ***Val***ProGluGlyAlaLeu*****PheAsnValTrpGluValGly***Asp*** | 404 |
| Db | 1164 | TACATGATTTCCGGCAACACGCTCTCTTCCTCAACTCTGTGTCATAGGGCGGAACCT | 1222 |
| OY | 405 | LysTrpTrpAspArgProSerGlu**ArgProGluArgPheLeuGluThr**AlaGlu | 424 |
| Db | 1224 | AAATATCGGACACTACCCGACGCGCTTCCAGCCGAGAGGTTTCTGGAGAAG----- | 1274 |
| OY | 425 | GlyGluAla*****LeuAspLeuArgGly**HisPheGlnLeuLeuProPheGlySer | 444 |
| Db | 1275 | --GMAAAGCGCCGACATGATGTTAAAGGCGACGATTTTGACGTGCTACCTTCGGAA | 1331 |
| OY | 445 | GlyArg**MetCysProGlyVal***LeuAlaThrSerGly***AlaThrLeuLeuAla | 464 |
| Db | 1332 | GGCAGGAGAGCGCTCCCGAGGATCTTTTACCATTCCAGAGGAGGTGCATCATAAATTGG | 1391 |
| OY | 465 | SerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGlnIleLeuLysGly | 484 |
| Db | 1392 | ACGATGATTCATGCTTCGATTGGAAAGCTG-----CCGACGGG----- | 1430 |
| OY | 485 | **AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValProArgAlaHisSer | 504 |
| Db | 1431 | --TCGCGCCATGTGATATATGACAGACGCGCAGGCGCTCACGGACCGCGAGACCGAT | 1487 |
| OY | 505 | LeuValCysValProLeuAlaArgIle | 513 |
| Db | 1488 | TTGTTTTCCTGCTGTGCTCCGCGAAGTT | 1514 |

RESULT 13

US-10-411-225-7

Sequence 7, Application US/10411225

Publication No. US20040261146A1

GENERAL INFORMATION

APPLICANT: Kasumi, Takaaki

APPLICANT: Ayabe, Shin-ich

APPLICANT: Akashi, Tomoyos

1. TITLE OF INVENTION: Genes C

FILE REFERENCE: 001560-383

CURRENT APPLICATION NUMBER

CURRENT FILING DATE: 2003-04-11
 PRIOR APPLICATION NUMBER: IIS/09/673 785

PRIOR FILING DATE: 2000-09-29

PRIOR APPLICATION NUMBER: PCT/JP00/04379

PRIOR FILING DATE: 2000-01-30

PRIOR APPLICATION NUMBER: PCT/JP00/00490

PRIOR FILING DATE: 1999-01-28

PRIOR APPLICATION NUMBER: JP 11-205229

PRIOR FILING DATE: 1999-01-19
PRIOR APPLICATION NUMBER: JP 11-22427

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PatentIn version 3.0

; SEQ ID NO 7

; LENGTH: 1770

```

;
TYPE: DNA
CCACTTTC - 25111 - 451000000

```

ORGANISM: *Pellia lucescens*

OTHER INFORMATION: Nucleotide sequence

1
 2
 3
 4
 5
 6
 7
 8
 9
 10
 11
 12
 13
 14
 15
 16
 17
 18
 19
 20
 21
 22
 23
 24
 25
 26
 27
 28
 29
 30
 31
 32
 33
 34
 35
 36
 37
 38
 39
 40
 41
 42
 43
 44
 45
 46
 47
 48
 49
 50
 51
 52
 53
 54
 55
 56
 57
 58
 59
 60
 61
 62
 63
 64
 65
 66
 67
 68
 69
 70
 71
 72
 73
 74
 75
 76
 77
 78
 79
 80
 81
 82
 83
 84
 85
 86
 87
 88
 89
 90
 91
 92
 93
 94
 95
 96
 97
 98
 99
 100
 101
 102
 103
 104
 105
 106
 107
 108
 109
 110
 111
 112
 113
 114
 115
 116
 117
 118
 119
 120
 121
 122
 123
 124
 125
 126
 127
 128
 129
 130
 131
 132
 133
 134
 135
 136
 137
 138
 139
 140
 141
 142
 143
 144
 145
 146
 147
 148
 149
 150
 151
 152
 153
 154
 155
 156
 157
 158
 159
 160
 161
 162
 163
 164
 165
 166
 167
 168
 169
 170
 171
 172
 173
 174
 175
 176
 177
 178
 179
 180
 181
 182
 183
 184
 185
 186
 187
 188
 189
 190
 191
 192
 193
 194
 195
 196
 197
 198
 199
 200
 201
 202
 203
 204
 205
 206
 207
 208
 209
 210
 211
 212
 213
 214
 215
 216
 217
 218
 219
 220
 221
 222
 223
 224
 225
 226
 227
 228
 229
 230
 231
 232
 233
 234
 235
 236
 237
 238
 239
 240
 241
 242
 243
 244
 245
 246
 247
 248
 249
 250
 251
 252
 253
 254
 255
 256
 257
 258
 259
 260
 261
 262
 263
 264
 265
 266
 267
 268
 269
 270
 271
 272
 273
 274
 275
 276
 277
 278
 279
 280
 281
 282
 283
 284
 285
 286
 287
 288
 289
 290
 291
 292
 293
 294
 295
 296
 297
 298
 299
 300
 301
 302
 303
 304
 305
 306
 307
 308
 309
 310
 311
 312
 313
 314
 315
 316
 317
 318
 319
 320
 321
 322
 323
 324
 325
 326
 327
 328
 329
 330
 331
 332
 333
 334
 335
 336
 337
 338
 339
 340
 341
 342
 343
 344
 345
 346
 347
 348
 349
 350
 351
 352
 353
 354
 355
 356
 357
 358
 359
 360
 361
 362
 363
 364
 365
 366
 367
 368
 369
 370
 371
 372
 373
 374
 375
 376
 377
 378
 379
 380
 381
 382
 383
 384
 385
 386
 387
 388
 389
 390
 391
 392
 393
 394
 395
 396
 397
 398
 399
 400
 401
 402
 403
 404
 405
 406
 407
 408
 409
 410
 411
 412
 413
 414
 415
 416
 417
 418
 419
 420
 421
 422
 423
 424
 425
 426
 427
 428
 429
 430
 431
 432
 433
 434
 435
 436
 437
 438
 439
 440
 441
 442
 443
 444
 445
 446
 447
 448
 449
 450
 451
 452
 453
 454
 455
 456
 457
 458
 459
 460
 461
 462
 463
 464
 465
 466
 467
 468
 469
 470
 471
 472
 473
 474
 475
 476
 477
 478
 479
 480
 481
 482
 483
 484
 485
 486
 487
 488
 489
 490
 491
 492
 493
 494
 495
 496
 497
 498
 499
 500
 501
 502
 503
 504
 505
 506
 507
 508
 509
 510
 511
 512
 513
 514
 515
 516
 517
 518
 519
 520
 521
 522
 523
 524
 525

OTHER INFORMATION: activity to directly convert flavanone to flavone

US-10-411-225-7

Alignment Scores:

| | |
|------------|-----------|
| Pred. No.: | 5.44e-123 |
|------------|-----------|

Length: 1770

Score:

Matches: 190

Percent Similarity

Conservative: 91

Best Local Similarity

Mismatches: 183

Query Match:

Inde18: 25

DB:

Gaps: 8

US-09-857-581B-66 (1-521) x US-10-411-225-7 (1-1770)

| | | | |
|----|-----|--|------|
| QY | 33 | ProAsnProProSerPro***ProAglLeuProPheIleGlyHis***HisLeuLeuLys | 52 |
| Db | 99 | CCCTACCTCCCGGGCGGTCCCT---CTCCCATCATGGGCCCATTTACACCTCTCCGGG | 1555 |
| QY | 53 | AspLysLeuLeuHisTyrAla***IleAspLeuSerLysHisGlyProLeuPheSer | 72 |
| Db | 156 | CCGAGA---CTCCACCAAAACCTTCCACGATCTGTCCCAAGCGTAAAGGCCCTTAAATGCAG | 212 |
| QY | 73 | *****PheGlySerMetProThrValValAlaSerThrProGluLeuPheLysLeuPhe | 92 |
| Db | 213 | CTCCGCGCTCGGGTCCATCCGCTGCGCATTTGCTGCTCCGCCGAGAGCTCGGCAAGAAATGC | 272 |
| QY | 93 | LeuGln*****GluAlaThrSerPhe***ThrArgPheGlnThrSerAla***Arg*** | 112 |
| Db | 273 | CTCAAGACACACAGAGCTGCTGC---TTCTCTCTCCCGAAACACTCCACCGCCATTGATATC | 329 |
| QY | 113 | LeuThrTyrAsp*****ValAla*****Pro***GlyProTyrTrp***PheValArg | 132 |
| Db | 330 | GTCACCTCATGATTCATCCCTCGCTTCTCTCCCTACGGGGCTTACGTGAATTCATCAAG | 389 |
| QY | 133 | LysLeuIleMetAsnAspLeu***AsnAlaThrThrValAsn***LeuArgProLeuArg | 152 |
| Db | 390 | AAATTATGCACTCAGAGCTGCTCGGGGCCCAAAATCTGCCCATCTTACGCCATACGG | 449 |
| QY | 153 | ThrGlnGlnIleArgLys***LeuArg***MetAlaGln***AlaGluAla***LysPro | 172 |
| Db | 450 | ACTCTCGAAGTCAAGCTTCTTCTCCAAATTCATTATGGCCAAAGGTGAAATCGGGGAGAGC | 509 |
| QY | 173 | LeuAsp***ThrGluGluLeuLeuLysTrp***AsnSerThr***SerMetMet***Leu | 192 |
| Db | 510 | TTCAACGTGACAGAGAGCTCGTGAAGCTGACAGCAACCTCATATCTGCATATGATGCTG | 569 |
| QY | 193 | -----GlyGluAlaGluGluIleArgAspIleAlaArgGlu | 204 |
| Db | 570 | AGCATACGATGTTCAAGACGAGCTCGAGGCCGAGCGCGGACGAGCGATTCGGGAG | 629 |
| QY | 205 | ValLeuLysIle***GlyGluTyrSerLeuThrAspPheIle***ProLeuLys***Leu | 224 |
| Db | 630 | GTCACGCAATATTTGGGAGTTCCAGACGTCTCCGACATCATATGAGCTTTGTAAGAACTTC | 689 |
| QY | 225 | LysValGlyLysTyrGluLysArgIleAspAspIleLeuAsnLysPheAspProValVal | 244 |
| Db | 690 | GATTTCCAAAGTAAAGAAAGCGCTCCGAGATATCCAGAGAAATATGATGCTCTGCTG | 749 |
| QY | 245 | GluArgValIleLysLysArgAlaG***IleValArgArgArg***AsnGlyGlu***** | 264 |
| Db | 750 | GAGAGATCATCATCCGACAGAGAGAG---CAAGGCGGACCCAGCGCGCGGTGGC | 803 |
| QY | 265 | GluGlyGlu***SerGlyVal***LeuAspThrLeuLeuGluPheAlaGluAspGluThr | 284 |
| Db | 804 | GCGCGCGGGAGGCCAAGATTTTCTTGACATGTCTCTCCACATTAATGAGAGCGGGAAA | 865 |
| QY | 285 | ***GluIleLysIleThrLys*****Ile***GlyLeuValValAsp***PheSerAla | 304 |
| Db | 864 | GCCGAAGTTAAATTCAGAGGAGCATCTAAAGCTTTGATCTGGAGTTCTTCACCGCC | 922 |
| QY | 305 | Gly***AspSerThrAla*****ThrGluTrpAlaLeuAlaGluLeuIleAsnAsnPro | 324 |
| Db | 924 | GGCACCGACAGCAGCGCGATCGGTGTGAATGGCGCGATACAGAAAGATCAACAAATCCA | 983 |

```

QY 325 ***Valleu*****Alaarglunlu***TyserValValglylyAsp***LeuVal 344
      |||||
Db 984 AATGTGTGAAGAAAGCTCAAGAGATTGGCCAACTGTCTGGATTCCACAGATTCTG 1043
QY 345 AspgluValAspTrglnAsnleuProTyrTleargAlaIleVallysgIuTrpPhearg 364
      |||||
Db 1044 CAAGATCCGACGGCCCAANTCTGCCTTACCTTCACCCCTCATCAAGAAACCTTCGG 1103
QY 365 MethisProPleuProValVallyArglyLeCys**Glunlucys***Ileasnly 384
      ::::::::::::::::::::
Db 1104 CTCACCCCTCAATCCCAATGCTGGCAGAGAAATCGATCTCCGACTCGTCATCGACGGC 1163
QY 385 ***Val**ProglunlyAlaleu*****PheasnValTrpGlnValgly***Asp*** 404
      ::::::::::::::::::::
Db 1164 TACATGATTCGGGCCAACACGCTGCTCTTCGTCAACCTCTGTTCATGGGCGGACCT 1223
QY 405 LysTyrTrpAspArgProSerGlu**ArgProGluArgPheleuGluTrp***AlaGlu 424
      |||||
Db 1224 AAAATCTGGACTACCCGACGGCGCTTCACCGGAGAGCTTCTCGAGAG----- 1274
QY 425 Glylunla*****LeuAspLeuArgGly***HisPheGlnleuLeuProPheGlySer 444
      ::::::::::::::::::::
Db 1275 ---GAAAAAGCGCGCATCGATGTTAAAGGCGACAGATTGAGCTGCTACCGCTTCGAGAC 1331
QY 445 GlyArg**MetCysProGlyVal**LeuAlaThrSerGly***AlaThrLeuAla 464
      |||||
Db 1332 GGCAGAGAGGCTCCCGAGGATGCTTTTtAGCATTCAGAGAGGTGGTCATCATATTGGG 1391
QY 465 SerleuileGlnCysPheAspLeuGlnValleuGlyProGlnlyGlnIleleuLysGly 484
      |||||
Db 1392 ACGATGATTCATGCTCTCGATTGGAGCTG-----CCGACGGC----- 1430
QY 485 **AspAlaLysValSerMetGluGlnArgAlaGlyleuThrValProAlaIleHisSer 504
      |||||
Db 1431 --TCCGCGCATGTTGATGATGSCAGAACGGCGCAGGCTCAACGCCACCGAGAGACCGAT 1487
QY 505 LeuValCysValProleuAlaArgIle 513
Db 1488 TTGTTTTCCTGCTGTGTGCGCGAGTT 1514

RESULT 14
US-10-424-599-6882
; Sequence 6882, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 6882
; LENGTH: 1841
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_106222C.1
US-10-424-599-6882

Alignment Scores:
Pred. No.: 1,13e-122 Length: 1841
Score: 919.50 Matches: 198
Percent Similarity: 57.14% Conservative: 86
Best Local Similarity: 39.84% Mismatches: 184
Query Match: 38.49% Indels: 29
Gaps: 9

US-09-857-581B-66 (1-521) x US-10-424-599-6882 (1-1841)

```



```

Db      350 ACCCGAATACTCACTTCCAAACCGCCCGCCAAACCTCCCTTAAGGCTTAGCC 409
Qy      115 TyrAsp*****ValAla*****Pro**GlyProTyrTrp**PheVal 131
Db      410 TACGATATCCCAAGACTTCTCTTTTCGGTTTGCACTTCGACCTTACCTGAGAGTTCAAG 469
Qy      132 ArgGlyLeuLleMetAsnAspLeu***AsnAlaThrThrValAsn**LeuArgProLeu 151
Db      470 AAGAAACTCTGCAATGTCGAGCTTCTCAGCGCCGAATGATGAGCAAGTTCCTCCCGT 529
Qy      152 ArgThr-GlnGlnLleArgLys**LeuArg**MetAlaGln**AlaGluLys**Iy 171
Db      530 AGGCTAGCAAGAGACCAAGAGATTCATCAGCCCGCGTTCGAAAAGAGATCCCGCGCA 569
Qy      171 sProLeuAsp**ThrGluGluLeuLeuLysTrp**AsnSerThr**SerMetCet** 191
Db      590 GGCCTGTGATTCGAGACGAGCTCATGACACTCTCCACACATCGTATCCAGAAATGAC 649
Qy      191 *Leu-----GlyGluAlaGluLleArgAspLleAlaIar 203
Db      650 GCTGAGTCAAGAGACTTCTGAGAACGAAACAGGCTGAGAGATGAGAGAGCTCGTGC 709
Qy      203 gGluValLeuLysIle**GlyGluTyrSerLeuThrAspPheIle**ProLeuLys** 223
Db      710 GAATATCGGGAGACTCATGGGGAAGTTCAACGTTTGGACTTCATTGTCATCTGAAGCC 769
Qy      223 *LeuLysValGlyLysTyrGluLysArgLleAspAspLleLeuAsnLysPheAspProVa 243
Db      770 TTTGATTTGACAGGGGTTCAACAAAAATCAAGGAGACTCGGGACAGGTTTGACGTTGT 829
Qy      243 lValGluArgValLleLysLysArgArg***IleValArgArgArg**AsnGlyGlu** 263
Db      830 GGTGACGGGATATATAAGCAGCTCAGAG-----GAAAGAGGAAAAACAAGAAAC 883
Qy      263 ***GluGlyGlu**SerGlyVal**LeuAspThrLeuLeuGluPheAlaGluAspGl 283
Db      884 GGGCAGACGACCGTCAGTTTAAGATATGCTGATGTTTATTTGAGACTTAGCGAAGATGA 943
Qy      283 uThr***GluLleLysLleThrLys*****Ile**GlyLeuValValAsp**PheSe 303
Db      944 CAGTTCTGAATCAAAATTAACCAAGAAAAATTAAGCCTTCATCATGATATATTTGT 1003
Qy      303 rAlaGly***AspSerThrAla*****ThrGluTPrAlaLeuAlaGluLeuLleAsnAs 323
Db      1004 TGCCTGGAGACTGACACGTCAGCTGCACATGAGATGGGCTATGGCCAGAGTTAATCAACAA 1063
Qy      323 nPro***ValLeu*****AlaArgGluGlu**TyrSerValValGlyLysAsp**Le 343
Db      1064 TCCATATGTGTTGGAGAGGCAAGGCAAGGAGATAGATGCGGTGGTGAAGAAAGTAGAAT 1123
Qy      343 uValAspGluValAspThrGlnAsnLeuProTyrLleArgAlaLleValLysGluThrPh 363
Db      1124 GGTAGAGAGATCAGATATTCACCACTTCTTACCTTCAGACCATTTGTAGAGAAACACT 1183
Qy      363 eArgMetHisProProLeuProValValLysArgLysCys**GluGluCys***IleAs 383
Db      1184 TAGGCTTCACCCAGGTGCTCATTTGTTAGAGAAATCATCAAAAAGTCCGGTGGTTTG 1243
Qy      383 nGly***Val**ProGluGluValaLeu*****PheAsnValTrpGluValGly**As 403
Db      1244 TGGGTATGATATTCAGCAAAAGACTCGATATTTGTCAATGTTTGGGCTATTTGGTAGGA 1303
Qy      403 p***LysTyrTrpAspArgProSerGlu**ArgProGluArgPheLeuGluThr**Al 423
Db      1304 TCCCAATCACTGGAGAAACCTTTTGAGTTTAGGCCAGAGAGGTTTATCAGA----- 1355
Qy      423 aGluGlyGluAla*****LeuAspLeuArgGly**HisPheGlnLeuLeuProPheGl 443
Db      1356 -GATGGGCAA--AATCAATTGATGTAGGGGCAACATTATCATTTTATTCATTGG 1411
Qy      443 ySerGlyArg**MetCysProGlyVal**LeuAlaThrSerGly**AlaThrLeuLe 463

```

```

Db      1412 GAGTGAAGAAAGACGTGCGCTGTGCTTCTTACGCTGGCAGGTTGCTGTGAATCT 1471
Qy      463 uAlaSerLeuLleGlnCysPheAspLeuGlnValLeuGlyProGlnGluLleLeuLys 483
Db      1472 GGTATATATTAATTCATATGTTTCAATGGAAGCTGTGTGGCAATGGC----- 1520
Qy      483 sGly**AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValProArgAlaH 503
Db      1521 -----MAGTGGACATGGAAGAAAGTCTGGCATCACTCTCCGAGGGCTAA 1567
Qy      503 sSerLeuValCysValProLeuAlaArgIle 513
Db      1568 CCCCATATTTGTGTCTCTGTCCAAAGGATT 1598

```

Search completed: December 22, 2005, 02:36:31
 Job time : 1016 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Comphen Ltd.

OM protein - protein search, using sw model

Run on: December 22, 2005, 00:03:14 / Search time 44 Seconds
(without alignments)
84.451 Million cell updates/sec

Title: US-09-857-581b-66
Perfect score: 2389
Sequence: 1 MLEFALGLXVLAFLXHLR.....AHLVCPVLRIGVASKLLS 521

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 53982 seqs, 7132107 residues

Total number of hits satisfying chosen parameters: 53982

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Published Applications AA New:
1: /cgn2_6/prodata/2/pubppaa/US08_NEW_PUB pep:*
2: /cgn2_6/prodata/2/pubppaa/US06_NEW_PUB pep:*
3: /cgn2_6/prodata/2/pubppaa/US07_NEW_PUB pep:*
4: /cgn2_6/prodata/2/pubppaa/PCT_NEW_PUB pep:*
5: /cgn2_6/prodata/2/pubppaa/US09_NEW_PUB pep:*
6: /cgn2_6/prodata/2/pubppaa/US10_NEW_PUB pep:*
7: /cgn2_6/prodata/2/pubppaa/US11_NEW_PUB pep:*
8: /cgn2_6/prodata/2/pubppaa/US60_NEW_PUB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|--------------------|--------------------|
| 1 | 398 | 16.7 | 524 | US-10-667-295-207 | Sequence 207, App |
| 2 | 398 | 16.7 | 531 | US-10-667-295-206 | Sequence 206, App |
| 3 | 398 | 16.7 | 540 | US-10-667-295-205 | Sequence 205, App |
| 4 | 387.5 | 16.2 | 506 | US-10-667-295-140 | Sequence 140, App |
| 5 | 387.5 | 16.2 | 526 | US-10-667-295-139 | Sequence 139, App |
| 6 | 381.5 | 16.0 | 505 | US-10-667-295-82 | Sequence 82, App |
| 7 | 381.5 | 16.0 | 534 | US-10-667-295-81 | Sequence 81, App |
| 8 | 327 | 13.3 | 434 | US-10-667-295-141 | Sequence 141, App |
| 9 | 317 | 13.3 | 433 | US-10-667-295-83 | Sequence 83, App |
| 10 | 240.5 | 10.1 | 502 | US-10-821-234-1554 | Sequence 1554, App |
| 11 | 226.5 | 9.5 | 504 | US-10-131-826A-64 | Sequence 64, App |
| 12 | 191 | 8.0 | 524 | US-11-102-240-54 | Sequence 54, App |
| 13 | 190 | 8.0 | 524 | US-11-000-463-877 | Sequence 877, App |
| 14 | 190 | 8.0 | 524 | US-11-000-463-878 | Sequence 878, App |
| 15 | 190 | 8.0 | 524 | US-11-000-463-879 | Sequence 879, App |
| 16 | 187 | 7.8 | 546 | US-11-000-463-805 | Sequence 405, App |
| 17 | 186.5 | 7.8 | 490 | US-10-507-106-2 | Sequence 2, App |
| 18 | 183 | 7.7 | 568 | US-11-000-463-806 | Sequence 406, App |
| 19 | 181 | 7.6 | 468 | US-10-957-569-28 | Sequence 28, App |
| 20 | 181 | 7.5 | 520 | US-10-995-561-598 | Sequence 598, App |
| 21 | 179.5 | 7.5 | 520 | US-10-667-295-250 | Sequence 250, App |
| 22 | 178.5 | 7.5 | 520 | US-10-995-561-597 | Sequence 597, App |
| 23 | 178.5 | 7.5 | 520 | US-10-995-561-599 | Sequence 599, App |
| 24 | 175.5 | 7.3 | 429 | US-11-000-463-407 | Sequence 407, App |
| 25 | 161.5 | 6.8 | 503 | US-10-821-234-1527 | Sequence 1527, App |

| | | | | | |
|----|-------|-----|------|--------------------|--------------------|
| 26 | 158 | 6.6 | 524 | US-10-507-106-4 | Sequence 4, App |
| 27 | 157 | 6.6 | 509 | US-10-131-826A-108 | Sequence 108, App |
| 28 | 155 | 6.5 | 498 | US-10-667-295-249 | Sequence 249, App |
| 29 | 150.5 | 6.3 | 347 | US-11-186-284-226 | Sequence 226, App |
| 30 | 142.5 | 6.0 | 521 | US-10-821-234-1546 | Sequence 1546, App |
| 31 | 103.5 | 4.3 | 147 | US-10-667-295-39 | Sequence 39, App |
| 32 | 103.5 | 4.3 | 404 | US-10-497-135-3 | Sequence 3, App |
| 33 | 100.5 | 4.2 | 404 | US-10-497-135-4 | Sequence 4, App |
| 34 | 97.5 | 4.1 | 406 | US-11-075-185-23 | Sequence 23, App |
| 35 | 84.5 | 3.5 | 386 | US-10-497-135-20 | Sequence 20, App |
| 36 | 83 | 3.5 | 388 | US-10-497-135-19 | Sequence 19, App |
| 37 | 78 | 3.3 | 397 | US-11-143-980-51 | Sequence 51, App |
| 38 | 71.5 | 3.0 | 1976 | US-11-069-834-54 | Sequence 54, App |
| 39 | 69.5 | 2.9 | 638 | US-10-488-517-260 | Sequence 260, App |
| 40 | 69.5 | 2.9 | 1652 | US-10-995-561-661 | Sequence 661, App |
| 41 | 69.5 | 2.9 | 1938 | US-10-995-561-661 | Sequence 661, App |
| 42 | 69.5 | 2.9 | 1938 | US-10-995-561-662 | Sequence 662, App |
| 43 | 69.5 | 2.9 | 1954 | US-10-995-561-660 | Sequence 660, App |
| 44 | 69.5 | 2.9 | 1972 | US-10-995-561-664 | Sequence 664, App |
| 45 | 69.5 | 2.9 | 1972 | US-10-995-561-666 | Sequence 666, App |

ALIGNMENTS

RESULT 1
US-10-667-295-207
Sequence 207, Application US/10667295
Publication No. US20050257293A1
GENERAL INFORMATION:
APPLICANT: Mascia, Peter
TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
FILE REFERENCE: 11696-047001
CURRENT APPLICATION NUMBER: US/10/667,295
PRIOR FILING DATE: 2003-09-17
PRIOR APPLICATION NUMBER: US 60/411,823
NUMBER OF SEQ ID NOS: 263
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 207
LENGTH: 524
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(524)
OTHER INFORMATION: Ceres Seq. ID no. 12450443
US-10-667-295-207

| | | | | |
|-----------------------|-----------------|---|-----------|------------|
| Query Match | 16.7% | Score 398 | DB 6 | Length 524 |
| Best Local Similarity | 27.1% | Pred. No. 2e-37 | | |
| Matches 132 | Conservative 77 | Mismatches 220 | Indels 58 | Gaps 18 |
| QY | 35 | PSPPXRLPFGHXLKXKLYAKIDSKKHGPFSSXFGSMPTVVASTPELFLFIQ | 94 | |
| DB | 52 | PPGP-PAVVPFGNVLQVGNLNRFLARISARGPVRLRLGRLVVSDFPLAEVTH | 110 | |
| QY | 95 | XXEATSFYTRFQTSAXRXLTYDXVA-----XXPYGPMXFEVKLIMNDLNATVNXL | 148 | |
| DB | 111 | -TGVFFGSR-----PRNVFDLFTANGADMVTEVGDHMRRRRWTLPPFARVVOQ | 164 | |
| QY | 149 | RPLRTOQIRKRLKXMAOKXBAKKPLDYTEEL-LKXNSTXSMXKLGAEARIR----- | 200 | |
| DB | 165 | RGWWEAEMLDAVDSAAQRAAGLVRRRLQMLNIMYGMFDPARFGSVDDPMEVEAT | 224 | |
| QY | 201 | ---IAEVLKIXEYSLTFPIKXKLVKGYEKRIIDI---LNKEDPVEVIRKRRX | 253 | |
| DB | 225 | RNSERSRLAQSFVYGDPIVLRPLKQ-YLARKCDLQARLAFN---SNVEKRRK | 280 | |
| QY | 254 | IVRRKNGEXXEGXGVXLDLLEFAEDETXIKITKXXIXGLVVDXPSAGXSTPAXXT | 313 | |
| DB | 281 | VM-----DAPDDKQKLR-CAIDHVLQ-AEKSG---ETTPERVIVYVENINVAIETLMSI | 331 | |

```

QY      31  EMLLAELINNPXYLXXAREXYSVGKXLDVENDTONPYRAIVKTEPFMHPELP-VV 3172
Db      332  EMLLAENVNHPAVQRYKVRDEIKAVVADHEPTESTITHRPYIQAVIKETLHPILV 391
QY      373  KRKCXEBCKINGVXPEGALXXFNVQVQXDKKYNDPSEKXPERFLETTXAEAGAXXLDL 432
Db      392  PHNNLEBAKLCGTTIKSGSKVYVNMAMWLNANNEIMDKDBEPFPRFFL-----GEKSVDA 446
QY      433  R---GXHFQILLPRGSGRMCPGVXLATSGXATLLASLIQCDFDLOVLGFQGOILKGXDAKV 488
Db      447  TVGSKYDFRFLPFGVGRBSCPGIITALLPITALIVGLKLVRSFEM--VPPPGV-----EKL 498
QY      490  SMEERAG 496
Db      499  DVSEKGS 505

```

```

RESULT 2
US-10-667-295-206
; Sequence 206, Application US/10667295
; Publication No. US20050257293A1
; GENERAL INFORMATION:
; APPLICANT: Mascia, Peter
; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
; FILE REFERENCE: 11696-047001
; CURRENT APPLICATION NUMBER: US/10/667,295
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,823
; PRIOR FILING DATE: 2002-09-17
; NUMBER OF SEQ. ID NOS: 263
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ. ID NO 206
; LENGTH: 531
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(531)
; OTHER INFORMATION: Ceres Seq. ID no. 12450442
; US-10-667-295-206

```

[illegible]

```

Oy      433 R---GXHPDLPFGSGRXKCPGVXLATGSGXATTLIASIIQCEDLVLPQCGIIXGXDAKV 489
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      454 TVGKXKDFPFLPFVGRSGRCPIIILALILALIVGLKVRSEW---VPPGV-----EKL 505

Oy      490 SMERAG 496
        : : |
Db      506 DYSEKGG 512

```

```

RESULT 3
US-10-667-295-205
; Sequence 205, Application US/10667295
; Publication No. US20050257293A1
; GENERAL INFORMATION:
; APPLICANT: Mascia, Peter
; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
; FILE REFERENCE: 11696-047001
; CURRENT APPLICATION NUMBER: US/10/667,295
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,823
; PRIOR FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 263
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 205
; LENGTH: 540
; TYPE: PR1
; ORGANISM: Zea mays
; FEATURES:
; NAME/KEY: VARIANT
; LOCATION: (1)...(540)
; OTHER INFORMATION: Ceres Seq. ID no. 12450441
US-10-667-295-205

```

| | | | | |
|-----------------------|--------------|---|-----------------|-------------|
| Query Match | 16.7%; | Score 398; | DB 6; | Length 540; |
| Best Local Similarity | 27.1%; | Pred. No. 2.1e-37; | | |
| Matches 132; | Conservative | 77; | Mismatches 220; | Indels 58; |
| Gaps | 18; | | | |
| QY | 35 | PPSPFXRLPFIGXHLTKDKLHYAXIDLSKKGRLFSXXXKSGMPTVASTPELLEKFLQ | 94 | |
| | | : : : : : : : : : : : : : : : : : : : : | | |
| DB | 68 | PPGF-PAVPVPGWMLQVGNLDNHRFLARLSARYGPRFLRLGVBNLVVSPDRPLATEVLH | 126 | |
| QY | 95 | XXEATSPKTRQTSAXKXLYDXVA-----XXPXPGRYAKFYVKLIMNDLXNATYVXKL | 148 | |
| | | : | | |
| DB | 127 | -TQGVFGRS-----PRVVFEDIFTAGADNVFTEYGDHMRMRVMTLPEFTGARVVQY | 180 | |
| QY | 149 | RPLTQOIRKKLRYMAQOAXEAXKFLDXTBEL-LTKXNXTSGMKLGEAEIRD----- | 200 | |
| | | : : : : : : : : : : : : : : : : : : : : | | |
| DB | 181 | KGMBAEADAAVSVAASAQRAAGLVVRRLOMLNIMGMMDARPGSVDDPMFEVAT | 240 | |
| | | : : : : : : : : : : : : : : : : : : : : | | |
| QY | 201 | --TAREVLKIXGEVSLTDFIXPKLKVGYEKRIIDI-----LNKEDPVERVYIKKRX | 253 | |
| | | : : : : : : : : : : : : : : : : : : : : | | |
| DB | 241 | RFSNRSRLASPFYNNGYDFIPLVLRPLRG-YLARCDOQARLAFN---SNVEKRRK | 296 | |
| | | : : : : : : : : : : : : : : : : : : : : | | |
| QY | 254 | IVRRXNGEXXEGEXSGVYLDTLLEFABDEFXEIKITKXXIXGLVNDXFSGXSTAXT | 313 | |
| | | : | | |
| DB | 297 | VM----PAPGDKGLR-CALDHVLQ-AEKSG---EITPENIYIVENINVAIETLMSI | 347 | |
| | | : : : : : : : : : : : : : : : : : : : : | | |
| QY | 314 | EWALAEILNNXVLXXAREEXYSVGKDXLDEVDTQNLPIYIRAIKVEPTFMHPPLP-VV | 372 | |
| | | : : : : : : : : : : : : : : : : : : : : | | |
| DB | 348 | EWALAEVNNHVAQVKRDEIKAVADVADHEPTTESTIHRPLPYLVITKTLRLHSBIFLVL | 407 | |
| | | : : : : : : : : : : : : : : : : : : : : | | |
| QY | 373 | KRKCEEXIXGXVYPEGALXFFVWVGXDKKWMDRPSSEKRPFRFLETAXGEGAXXLDL | 432 | |
| | | : : : : : : : : : : : : : : : : : : : : | | |
| DB | 408 | PHNMLEKLGYYIIPKGSKKVNVAMMLANNPELMDKREBRPRFL-----GEEKSDA | 462 | |
| | | : : : : : : : : : : : : : : : : : : : : | | |
| QY | 433 | R--GXHFQLLPSSGRXKCPGVXLATSGAATLIASLIQCPDLOYLQFOGQILKGDAXV | 489 | |
| | | : | | |
| DB | 463 | TVGKQVDFRFLPFGVGRSSCPGIIILPILALIVGLKVRSPEM--VBPBGV-----EKL | 514 | |
| | | : : : : : : : : : : : : : : : : : : : : | | |
| QY | 490 | SMERBAG 496 | | |
| | | : | | |
| DB | 515 | DVSEKGG 521 | | |

```

RESULT 4
US-10-667-295-140
; Sequence 140, Application US/10667295
; Publication No. US20050257293A1
; GENERAL INFORMATION:
; APPLICANT: Mascia, Peter
; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
; FILE REFERENCE: 11696-047001
; CURRENT APPLICATION NUMBER: US/10/667,295
; PRIOR APPLICATION NUMBER: 2003-09-17
; PRIOR FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 263
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 140
; LENGTH: 506
; TYPE: PR
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(506)
; OTHER INFORMATION: Ceres Seq. ID no. 13531807
US-10-667-295-140

Query Match
16.2%; Score 387.5; DB 6; Length 506;
Best Local Similarity 26.5%; Pred. No. 3e-36;
Matches 135; Conservative 73; Mismatches 227; Indels 75; Gaps 15;

QY 35 PPSXPRLPFIQXHLKDKLHYAXIDLSKKGPLFSXXFGSMPTVASTPELFKFLQ 94
DB 34 PPGPLP-VPIFGNMLQVGDIDLHNRNLTDLAKKFGDIFLLRMGQRNLVVSSPELAKEVHL 92
QY 95 XKEATSFYTRFQTSAXRXYTD-----XXVAXXKPGYVXFRKLIIMDLNATTVXKL 148
DB 93 -TQGVFSGR-----TRNVVFDIFGTGQDWFVTVYGGHMRKRRIM-----TVPF 138
QY 149 RLRLTQQR-----KXLRMAQXAEAKKPLDTEBLLKXNSTXSMXGLGEABE 197
DB 139 TNKVVOQYRHGSEEAADVCKNPDAAVSGTVIRRLQLMNTNMTIRIMEDRRFSE 198
QY 198 IRDIAREVLKIXG-----EYSLDFIXPLK-----XLKVGYEKRIIDILNKFPDV 243
DB 199 EDPILQRLALNGERSRLAQSFEVYVGFPIRLRPLKGYLKICEVETRLKLFQDYFV 258
QY 244 VERVIRKRRXIVRRXNGEXXGEXSGVXLDTLFEADETXEIKITKXXIXGLVVDXS 303
DB 259 DER--KKLGSTKSTNNNNE-----LKCAIDHILDAQRKGEINEDNVLIYVENINV 306
QY 304 AGDSTAXXTWMAELINNPVYLXXAREEXSVGKDXLVDEVDTONLPYIRAIYKETE 363
DB 307 AAIETTLMSIEWGIALVNHPEIQOKLRDEIDRVLAGHQVTEPDQKLPYLAQVVKETL 366
QY 364 RHMPLP-VVKRCKXEBXKXNGXVXPEGALXXFNWQVQXDXKXYWDRPSEKREPERLETX 422
DB 367 RLRLMALPLVPHNNLHDAKLGVDIPABSKILVNAMWLANNPAMWKKPBEFRPERFE-- 424
QY 423 AEGEAXXLDLRGXHFQLLPFGSGRXCPCGVXLTSGXATLLASLIQCFDVLQVGGQQL 482
DB 425 ---EESLVNANGNDPRYLPFGVGRSCPGIILALPLIGITLRLVONFEL--LPPGQ-- 477
QY 483 KXGDAVSMERAG---LTVPRASHLVCPV 509
DB 478 ----SQIDTSEKGGQFSHLHKLKSTIVAKP 503

```

```

; FILE REFERENCE: 11696-047001
; CURRENT APPLICATION NUMBER: US/10/667,295
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,823
; PRIOR FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 263
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 139
; LENGTH: 526
; TYPE: PR
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(526)
; OTHER INFORMATION: Ceres Seq. ID no. 13531806
US-10-667-295-139

Query Match
16.2%; Score 387.5; DB 6; Length 526;
Best Local Similarity 26.5%; Pred. No. 3.2e-36;
Matches 135; Conservative 73; Mismatches 227; Indels 75; Gaps 15;

QY 35 PPSXPRLPFIQXHLKDKLHYAXIDLSKKGPLFSXXFGSMPTVASTPELFKFLQ 94
DB 54 PPGPLP-VPIFGNMLQVGDIDLHNRNLTDLAKKFGDIFLLRMGQRNLVVSSPELAKEVHL 112
QY 95 XKEATSFYTRFQTSAXRXYTD-----XXVAXXKPGYVXFRKLIIMDLNATTVXKL 148
DB 113 -TQGVFSGR-----TRNVVFDIFGTGQDWFVTVYGGHMRKRRIM-----TVPF 158
QY 149 RLRLTQQR-----KXLRMAQXAEAKKPLDTEBLLKXNSTXSMXGLGEABE 197
DB 159 TNKVVOQYRHGSEEAADVCKNPDAAVSGTVIRRLQLMNTNMTIRIMEDRRFSE 218
QY 198 IRDIAREVLKIXG-----EYSLDFIXPLK-----XLKVGYEKRIIDILNKFPDV 243
DB 219 EDPILQRLALNGERSRLAQSFEVYVGFPIRLRPLKGYLKICEVETRLKLFQDYFV 278
QY 244 VERVIRKRRXIVRRXNGEXXGEXSGVXLDTLFEADETXEIKITKXXIXGLVVDXS 303
DB 279 DER--KKLGSTKSTNNNNE-----LKCAIDHILDAQRKGEINEDNVLIYVENINV 326
QY 304 AGDSTAXXTWMAELINNPVYLXXAREEXSVGKDXLVDEVDTONLPYIRAIYKETE 363
DB 327 AAIETTLMSIEWGIALVNHPEIQOKLRDEIDRVLAGHQVTEPDQKLPYLAQVVKETL 386
QY 364 RHMPLP-VVKRCKXEBXKXNGXVXPEGALXXFNWQVQXDXKXYWDRPSEKREPERLETX 422
DB 387 RLRLMALPLVPHNNLHDAKLGVDIPABSKILVNAMWLANNPAMWKKPBEFRPERFE-- 444
QY 423 AEGEAXXLDLRGXHFQLLPFGSGRXCPCGVXLTSGXATLLASLIQCFDVLQVGGQQL 482
DB 445 ---EESLVNANGNDPRYLPFGVGRSCPGIILALPLIGITLRLVONFEL--LPPGQ-- 497
QY 483 KXGDAVSMERAG---LTVPRASHLVCPV 509
DB 498 ----SQIDTSEKGGQFSHLHKLKSTIVAKP 523

```

```

RESULT 5
US-10-667-295-139
; Sequence 139, Application US/10667295
; Publication No. US20050257293A1
; GENERAL INFORMATION:
; APPLICANT: Mascia, Peter
; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM

```

```

RESULT 6
US-10-667-295-82
; Sequence 82, Application US/10667295
; Publication No. US20050257293A1
; GENERAL INFORMATION:
; APPLICANT: Mascia, Peter
; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
; FILE REFERENCE: 11696-047001
; CURRENT APPLICATION NUMBER: US/10/667,295
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,823
; PRIOR FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 263
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 82

```

```

; LENGTH: 505
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(505)
; OTHER INFORMATION: Ceres Seq. ID no. 12558791
US-10-667-295-82

Query Match          16.0%; Score 381.5; DB 6; Length 505;
Best Local Similarity 26.1%; Pred. No. 1.5e-35;
Matches 137; Conservative 82; Mismatches 236; Indels 69; Gaps 19;

Qy 1 MLELALGLXVALFXHLRPTXAXSKALRHLNPPSPXPRLPFIQHXHLLDKLLHYAX 60
Db 4 LLEKSL-----IAVAVAILATVISKLKRGKLLKLPFGPI-P-IPFGNMLQVGDIDLHNNL 58
Qy 61 IDLSKKHPLFSXXFGSMPTVVASTPELFLQXXEATSFYTRFQTSAXRLTYD---- 116
Db 59 VDYAKKFGDLFLRMGORNLVVSSPDLTKEVL-LTQVVEFGSR-----TRNVVFDITG 112
Qy 117 --XXVAXXPXGPYKFXFKLIMNDLXNATVYXKLRLRQOIRKKLR-XMAQXAEAXK-- 171
Db 113 KGQDMVFTVYGEHMKRRIM-----TVPFNNKVQNRBEGMEFEAASVVEDVKN 164
Qy 172 PLDYTE-----ELLKXNSTXSMXKLGAEIRDIAREVLKIXG-----EYSL 214
Db 165 PDSATKGIIVLRKRLQMMYNNMFRIMFDRPESEDDPLFLRLKALNGERSRLAQSFEYNY 224
Qy 215 TDFIXPLKXKLVGKYEKRIIDLINLKPDPYER-VIKKRXIVRRXNGEXXEGXSGVYL 273
Db 225 GDFILPLPRLG-YLKICQDVKDRRIALFKKYFVDERKQIASSKPTG---SEGKCAI 279
Qy 274 DTLLEFADETXEIKITKXXIXGLVVDXFSAGXDSTAXXTMALAEILNNPXVLXXARE 333
Db 280 DHILE-AEQKG---EINEDNVLIVENINVAIETLWSIEMGIAELVNHPEIQKLRNE 335
Qy 334 XYSVVGKXILVDEVDTONLPYIRAIKETFPMHPLP-VVKRCKEBCXKXVXPEGAL 392
Db 336 LDTVIGPQVQVTEPDLHLKPYLQAVVKETLRRLMAIPLVPHMMLHDATLAGYDIPABSK 395
Qy 393 XXFNWQVQGXKXKWDRESEKRPERPLETXABGEAXXLDLGRXHQQLLPFGSGRXMCPGV 452
Db 396 ILVNAWMLANNPNSWKKEEERPERFE-----ESHSVEANGNDRIYVPFGVGRSCPGI 450
Qy 453 XLATSGXATLTLASLIQCFDLOVLGPGQILKXDAKVSMEERAG 496
Db 451 ILALPILGITIGRMVQNFEL-LPPGQ-----SKVDTSKKG 486

RESULT 7
US-10-667-295-81
; Sequence 81, Application US/10667295
; Publication No. US20050257293A1
; GENERAL INFORMATION:
; APPLICANT: Masclia, Peter
; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
; FILE REFERENCE: 11696-047001
; CURRENT APPLICATION NUMBER: US/10/667,295
; PRIOR FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,823
; PRIOR FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 263
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81
; LENGTH: 534
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(534)
; OTHER INFORMATION: Ceres Seq. ID no. 12558790
US-10-667-295-81
```

```

Query Match          16.0%; Score 381.5; DB 6; Length 534;
Best Local Similarity 26.1%; Pred. No. 1.6e-35;
Matches 137; Conservative 82; Mismatches 236; Indels 69; Gaps 19;

Qy 1 MLELALGLXVALFXHLRPTXAXSKALRHLNPPSPXPRLPFIQHXHLLDKLLHYAX 60
Db 33 LLEKSL-----IAVAVAILATVISKLKRGKLLKLPFGPI-P-IPFGNMLQVGDIDLHNNL 87
Qy 61 IDLSKKHPLFSXXFGSMPTVVASTPELFLQXXEATSFYTRFQTSAXRLTYD---- 116
Db 88 VDYAKKFGDLFLRMGORNLVVSSPDLTKEVL-LTQVVEFGSR-----TRNVVFDITG 141
Qy 117 --XXVAXXPXGPYKFXFKLIMNDLXNATVYXKLRLRQOIRKKLR-XMAQXAEAXK-- 171
Db 142 KGQDMVFTVYGEHMKRRIM-----TVPFNNKVQNRBEGMEFEAASVVEDVKN 193
Qy 172 PLDYTE-----ELLKXNSTXSMXKLGAEIRDIAREVLKIXG-----EYSL 214
Db 194 PDSATKGIIVLRKRLQMMYNNMFRIMFDRPESEDDPLFLRLKALNGERSRLAQSFEYNY 253
Qy 215 TDFIXPLKXKLVGKYEKRIIDLINLKPDPYER-VIKKRXIVRRXNGEXXEGXSGVYL 273
Db 254 GDFILPLPRLG-YLKICQDVKDRRIALFKKYFVDERKQIASSKPTG---SEGKCAI 308
Qy 274 DTLLEFADETXEIKITKXXIXGLVVDXFSAGXDSTAXXTMALAEILNNPXVLXXARE 333
Db 309 DHILE-AEQKG---EINEDNVLIVENINVAIETLWSIEMGIAELVNHPEIQKLRNE 364
Qy 334 XYSVVGKXILVDEVDTONLPYIRAIKETFPMHPLP-VVKRCKEBCXKXVXPEGAL 392
Db 365 LDTVIGPQVQVTEPDLHLKPYLQAVVKETLRRLMAIPLVPHMMLHDATLAGYDIPABSK 424
Qy 393 XXFNWQVQGXKXKWDRESEKRPERPLETXABGEAXXLDLGRXHQQLLPFGSGRXMCPGV 452
Db 425 ILVNAWMLANNPNSWKKEEERPERFE-----ESHSVEANGNDRIYVPFGVGRSCPGI 479
Qy 453 XLATSGXATLTLASLIQCFDLOVLGPGQILKXDAKVSMEERAG 496
Db 480 ILALPILGITIGRMVQNFEL-LPPGQ-----SKVDTSKKG 515

RESULT 8
US-10-667-295-141
; Sequence 141, Application US/10667295
; Publication No. US20050257293A1
; GENERAL INFORMATION:
; APPLICANT: Masclia, Peter
; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
; FILE REFERENCE: 11696-047001
; CURRENT APPLICATION NUMBER: US/10/667,295
; PRIOR FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,823
; PRIOR FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 263
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 141
; LENGTH: 434
; TYPE: PRT
; ORGANISM: glycine max
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(434)
; OTHER INFORMATION: Ceres Seq. ID no. 13531808
US-10-667-295-141

Query Match          13.7%; Score 327; DB 6; Length 434;
Best Local Similarity 25.6%; Pred. No. 1.9e-29;
Matches 120; Conservative 68; Mismatches 207; Indels 74; Gaps 14;

Qy 76 GSMPTVASTPELFLQXXEATSFYTRFQTSAXRLTYD-----XXVAXXPXGPYKFX 129
Db 2 GORNLVVSSPELAEVLAH-LTQVVEFGSR-----TRNVVFDITGKGQDMVFTVYGEHMR 55
```

```

QY 130 FVRKLIIMNDLNAATVYXKRLPLRTOQIR-----KCLRMAOXAAXKPLDXTEE 178
Db 56 KRRIRIM-----TVPFPTTKVVOQYRHGSESEAAVVEDVKRNPDAVSGTVIRRLQ 107
QY 179 LTKMXNSTXMMXKLGAEIRIDIAREVLIKXG-----EYSLTDFIXPK-----XL 224
Db 108 LMWYNNMYIMFDRESEDEDPILQRLALNGERSRLAQSEFYNYGDFIPILRPFELKGLV 167
QY 225 KYGXEKRIIDILNKFDPVYERVIKGRXIYVRKXNGEXXEGXGVALDTLLEFADDT 284
Db 168 KICEKEKETRLKLFKQYFEDER--KRLGSKTSTNNNE-----LKCAIDHLLDQ 215
QY 285 XEIKITKXXIXGLVVDXFSAGDSTAXXTEMALAEIINNXYVLLXXAREXYSVNGKDXLV 344
Db 216 RKGELINEDVLYIVENINVAIETLWSTLEWGIABLNVHPEIQOKLRDIDVLGAGHOV 275
QY 345 DEVDTONLPYIRAIYKETERMHPPLP-VYKRCKXCECKXNGXVPEGALXXFNWQVQXD 403
Db 276 TEBDIOKLPYQAVVETIRLMAIPLVPHNMLHDAKLGVDIPAESKILVNAMWLANN 335
QY 404 XRYWDPSEKRPRLFETAYAGEAXXLDLRGAHFOLLPGSGRXMCPGYXLATSGAXATLL 463
Db 336 PAHWKKRBEFRPRPE-----EESLVEANGNDFRYLPFGVGRSCPGIILALPILGITL 390
QY 464 ASLQCFDQVLGPOQOILKGNAXKSMERAG--LTVBRAHSLVCPV 509
Db 391 GRLVONFEL--LPPPGQ-----SQIDTSEKGSQFSLHLIKSTIVAKP 431

RESULT 9
US-10-667-295-83
; Sequence 83, Application US/10667295
; Publication No. US2005025723A1
; GENERAL INFORMATION:
; APPLICANT: Maecia, Peter
; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
; FILE REFERENCE: 11696-047001
; CURRENT APPLICATION NUMBER: US/10/667,295
; PRIOR FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,823
; PRIOR FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 263
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 433
; TYPE: PRF
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(433)
; OTHER INFORMATION: Ceres Seq. ID no. 12558792
US-10-667-295-83

Query Match 13.3%; Score 317; DB 6; Length 433;
Best Local Similarity 25.6%; Pred. No. 2.5e-28; Indels 17;
Matches 115; Conservative 71; Mismatches 189;

QY 76 GSNMPTVASTPELFLQXXEATSFXTRPQTSAXRXLTYD-----XVAXXXEXGPYWX 129
Db 2 GORNLVVVSSPDLTKEVL-LTQVEFGSR-----TRNVVFDIFITGKGDWFWFYVGBHWR 55
QY 130 FVRKLIIMNDLNAATVYXKRLPLRTOQIRKXLR-XMAOXAAXK--PLDXTE-----E 178
Db 56 KRRIRIM-----TVPFPTTKVVOQYRHGSESEAAVVEDVKRNPDAVSGTVIRRLQ 107
QY 179 LTKMXNSTXMMXKLGAEIRIDIAREVLIKXG-----EYSLTDFIXPK-----XL 224
Db 108 LMWYNNMYIMFDRESEDEDPILRKLALNGERSRLAQSEFYNYGDFIPILRPFELKGLV 166
QY 230 EKRIIDILNKFDPVYERVIKGRXIYVRKXNGEXXEGXGVALDTLLEFADDEYKIEIK 288
Db 167 KICEKEKETRLKLFKQYFEDER-----SEGLKCAIDHLLT-AEQKG---E 218

```

```

QY 289 ITKXXIXGLVVDXFSAGDSTAXXTEMALAEIINNXYVLLXXAREXYSVNGKDXLVDEVD 348
Db 219 INEDVLYIVENINVAIETLWSTLEWGIABLNVHPEIQOKLRDIDVLGAGVOTEPD 278
QY 349 TONLPYIRAIYKETERMHPPLP-VYKRCKXCECKXNGXVPEGALXXFNWQVQDXKYM 407
Db 279 LHKRPYQAVVETIRLMAIPLVPHNMLHDAKLAGVDIPAESKILVNAMWLANNPRSM 338
QY 408 DRPSEKRPRLFETAYAGEAXXLDLRGAHFOLLPGSGRXMCPGYXLATSGAXATLLASLI 467
Db 339 KRPBEFRPRPE-----EESLVEANGNDFRYLPFGVGRSCPGIILALPILGITGMV 393
QY 468 QCFDQVLGPOQOILKGNAXKSMERAG 496
Db 394 QNFEL--LPPPGQ-----SKVDTSKGG 414

RESULT 10
US-10-821-234-1554
; Sequence 1554, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmant, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of preclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; PRIOR FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1554
; LENGTH: 502
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-821-234-1554

Query Match 10.1%; Score 240.5; DB 6; Length 502;
Best Local Similarity 22.3%; Pred. No. 1.5e-19; Indels 73; Gaps 20;
Matches 120; Conservative 83; Mismatches 261;

QY 6 ALGLXVLALEFXHLRPRP-----XAXSKALRHLPN--PSPXPRLPFIQXHLKDK 54
Db 4 AMGSLAALMAVYVHPRTLLGLTVAFLAADFLKRRPRKXVPPGPW-RLPFLGNFLVDFE 62
QY 55 LHYAXIDLSKKGHPLFSXXFGSMPTVASTPELFLQXXEATSFXTRPQTSAXRXL 114
Db 63 QSHLEVQVLPFKKYGKGNFSLJELGDISAVLITGLPLKEALIHMD-QNFGNR-PVTYPRBEH 120
QY 115 YDXXVAXXEXGPYWXVVRKLIIMNDLNAATVYXKRLPLRTOQIRKXLRMAO-XAAXK-- 171
Db 121 FKNGLIMSSGQAMKSORRFTLLALNPF-----GLGKSLERIOEERQHLTEAIKEE 173
QY 172 ---PLXTEBELKMXNSTXMMXKLGAEIRIDIAREVLIKXGEYSLTDFIXPKXKLVG 227
Db 174 NGQFPDPHFKINNVAISNITISIFGRPFVQDSWFOQLKLDDEVYLYLEASKTCQLYNVF 233
QY 228 KYEKRIIDILNKFDPVYERVI--KRRXIV-----RRXNGEXXEGXGVALDTLLE 278
Db 234 PW-----IMKLPFGHQTLFSNMKKLKLFSVSHMIDKHKDWNPAETRD---FIDAYLK 283
QY 279 FADDEYKE--IKTKXXIXGLVVDXFSAGDSTAXXTEMALAEIINNXYVLLXXAREXYS 336
Db 284 EMSKHTGNPTSGHEENLISCTIDLPFAGTETITSLRMLLYMALYLPLOEKVQAEIDR 343
QY 337 VVGKDXLVDEVDTONLPYIRAIYKETERMHPPLP-VYKRCKXCECKXNGXVPEGALXXF 395
Db 344 VIOGQGPQPTAARESMPTVAIVHEVQRMGNIIFLVNPREVTDTLAGYHLPRGTWILT 403

```



```
QY 109 AXRLTYDXVAXXP-----XGPYWXFVRKLIIMDLNATVNXKLRLPTQOIRKX 159
Db 128 -----LKWLGEGILLSGDDKMSRRR-----LTPAFHNLKSYIT-IFNKS 170
QY 160 LKXMAQ-----XAEAKKPLDXTBEILLKMXNSTXSMXKGEABE-IRDIAREVLKIXEYS 213
Db 171 ANIMLDKMHLSSESSRLDMFEHI-----SLMTLDSLOKCIFSPDSHCQERPEYI 222
QY 214 LTFDIXPLKXKLVKYEKRIIDILINKFP-----PVERVYIKKRX 253
Db 223 AT--LLELSAL-----VEKRSQHILQHMDFLYYLSHDGRRFHRACRLVHDFDAVIRERR 276
QY 254 IYRRXNGEXXGEGXSVXLD--TLLEFADETXEIKITKXXIXGLVVDXFSAGXDSTAX 311
Db 277 TLPTQIDIDFFKDKAKSKTLDFIDVLLSKDEGK-ALSDEDIRAEDTFMGCHDTTAS 335
QY 312 XTEWALAEILINNPXYLXXAREEXYSVGKXLVDEV--DTQNLPIYIRAIYKETPRMHP 368
Db 336 GLSWLYNLARHPEVOERCROGEVQELL-KDRDPKEIEMDDLQOLPFLTWCVESLRLHP 394
QY 369 LPVVRKCKXEECKI-NGXVXPEGALXXFNWQVGDXXKYWDPRSEKRPERFLETABEGBA 427
Db 395 APFISRCTQDIDLPPGRVYIPKGITCLLDIIGVHNHPTWPDPEVYDPFRFPENSKGRS 454
QY 428 XYLDRGXHFQLLPFGSGRXMCPGVXLATSGXATLLASLIQCF 470
Db 455 -----PLAFIPFSAGPRNCTIGQAFMAEMKVVALMLLHF 489

RESULT 13
US-11-000-463-877
; Sequence 877, Application US/11000463
; Publication No. US2005026423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; PRIOR FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 877
; LENGTH: 524
; TYPE: PRF
; ORGANISM: Homo sapiens
US-11-000-463-877
Query Match 8.0%; Score 190; DB 7; Length 524;
```

```
Best Local Similarity 22.0%; Pred. No. 9e-14;
Matches 115; Conservative 63; Mismatches 239; Indels 106; Gaps 21;
QY 1 MLELALGLXVLAUFHMLRPPXKSKRALRHLPPNPSXPRLPFIQXHL-----LKD 53
Db 20 LLLLVGSMWLA---RLAWTYAFYNNCRRLQCFPPQPKKNWFWGHLITPTREGLKD 76
QY 54 KLLHAXIDLSKKGGLPFSXXFGS-MPTVASTPELFLFLOXHA-----TSFXRPQTS 108
Db 77 -----STQMSATYSQGFVWLGPIIPFVLCHPDTIRISTNASAAAPKONLFTIRF--- 127
QY 109 AXRLTYDXVAXXP-----XGPYWXFVRKLIIMDLNATVNXKLRLPTQOIRKX 159
Db 128 -----LKWLGEGILLSGDDKMSRRR-----LTPAFHNLKSYIT-IFNKS 170
QY 160 LKXMAQ-----XAEAKKPLDXTBEILLKMXNSTXSMXKGEABE-IRDIAREVLKIXEYS 213
Db 171 ANIMLDKMHLSSESSRLDMFEHI-----SLMTLDSLOKCIFSPDSHCQERPEYI 222
QY 214 LTFDIXPLKXKLVKYEKRIIDILINKFP-----PVERVYIKKRX 253
Db 223 AT--LLELSAL-----VEKRSQHILQHMDFLYYLSHDGRRFHRACRLVHDFDAVIRERR 276
QY 254 IYRRXNGEXXGEGXSVXLD--TLLEFADETXEIKITKXXIXGLVVDXFSAGXDSTAX 311
Db 277 TLPTQIDIDFFKDKAKSKTLDFIDVLLSKDEGK-ALSDEDIRAEDTFMGCHDTTAS 335
QY 312 XTEWALAEILINNPXYLXXAREEXYSVGKXLVDEV--DTQNLPIYIRAIYKETPRMHP 368
Db 336 GLSWLYNLARHPEVOERCROGEVQELL-KDRDPKEIEMDDLQOLPFLTWCVESLRLHP 394
QY 369 LPVVRKCKXEECKI-NGXVXPEGALXXFNWQVGDXXKYWDPRSEKRPERFLETABEGBA 427
Db 395 APFISRCTQDIDLPPGRVYIPKGITCLLDIIGVHNHPTWPDPEVYDPFRFPENSKGRS 454
QY 428 XYLDRGXHFQLLPFGSGRXMCPGVXLATSGXATLLASLIQCF 470
Db 455 -----PLAFIPFSAGPRNCTIGQAFMAEMKVVALMLLHF 489

RESULT 14
US-11-000-463-878
; Sequence 878, Application US/11000463
; Publication No. US2005026423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; PRIOR FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
```

```

; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 878
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-878

Query Match      8.0%; Score 190; DB 7; Length 524;
Best Local Similarity 22.0%; Pred. No. 9e-14;
Matches 115; Conservative 63; Mismatches 239; Indels 106; Gaps 21;

QY 1 MLELALGLXVLALEFPHLRPTPXAXSKALRHLNPNPSPXPRLPFIQXHL-----LKD 53
DB 20 LLLLVGSMWLA---RIIAWTYAFYNNCRRLQCFPPQPKRWFWGHLGLITPTEGLKD 76
QY 54 KLLHYAXIDLSSKHGPLPSXFXGS-MPTVASTPELFLKFLQXXEA---TSFXTRFQTS 108
DB 77 -----STQMSATYSGCFVWMLGPIIPFVLCHPDTIRISITNASAAIAPKDLFIRF--- 127
QY 109 AKRXLITDXXVAXXP-----XGPYXKPVKRLIMNDLXNATVYXKLRLPTQOIRKX 159
DB 128 -----LKPWLGEGILLSGDCKWSRRHRM---LTPAFHFNILKSYIT--IFNKS 170
QY 160 LKXMAQ-----XAEAKKPLDXTTEELLKMXNSTXSMXKLGAEAE-IRDIAREVLKIXGEYS 213
DB 171 ANIMLDKMOHLASEGSSCLDMFEHI-----SLMTLDSLOKCIFFSPSHCOERPSEYI 222
QY 214 LTFPIXPFLKXKLVGKYEKRIDIDLKFP-----PVERVYIKKRX 253
DB 223 AT--LLELSAL---VEKRSQHILQHMDFLYLHSDGRFRHRCRLVHDFDAVIRERR 276
QY 254 IYRRXNGEXXGEXSGVXLD--TLLEPADETXEIKTKXXIXGLVVDXFSAGXDSTAX 311
DB 277 TLPFGIDDFKDKAKSKTLDIFDIVLLSKDBDGK-ALSDEDIIRADPTFMFGHDTTAS 335
QY 312 XTEWALAEIINNXYLXAXREXYSVVGKDXLVDEV---DTQNLPIRAIVKETFRMHP 368
DB 336 GLSWVLVNLARHPEYQERCRQEVQELL-KDRDPKEIEMWDLAQLPFLTWCVESIRLHP 394
QY 369 LPVVRKCKXEECKI-NGVXVPEGALXKFNWQVGDXXKYMDRPSXRPRLFETAAEGEA 427
DB 395 APFISRCTQDVLVLPDGRVTPKGITCLIDIIGVHNPTWMPDEYVDPFRFPENSKGS 454
QY 428 XLLDLRGXHFQLLPFGSGRXPMPGVXLTATSGXATLLASLIQCF 470
DB 455 -----PLAFIPPSAGPRNCIGQAFAMAEMKVIALMLLHF 489

RESULT 15
US-11-000-463-879
; Sequence 879, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Dimañac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; PRIOR FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623

```

```

; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 879
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-879

Query Match      8.0%; Score 190; DB 7; Length 524;
Best Local Similarity 22.0%; Pred. No. 9e-14;
Matches 115; Conservative 63; Mismatches 239; Indels 106; Gaps 21;

QY 1 MLELALGLXVLALEFPHLRPTPXAXSKALRHLNPNPSPXPRLPFIQXHL-----LKD 53
DB 20 LLLLVGSMWLA---RIIAWTYAFYNNCRRLQCFPPQPKRWFWGHLGLITPTEGLKD 76
QY 54 KLLHYAXIDLSSKHGPLPSXFXGS-MPTVASTPELFLKFLQXXEA---TSFXTRFQTS 108
DB 77 -----STQMSATYSGCFVWMLGPIIPFVLCHPDTIRISITNASAAIAPKDLFIRF--- 127
QY 109 AKRXLITDXXVAXXP-----XGPYXKPVKRLIMNDLXNATVYXKLRLPTQOIRKX 159
DB 128 -----LKPWLGEGILLSGDCKWSRRHRM---LTPAFHFNILKSYIT--IFNKS 170
QY 160 LKXMAQ-----XAEAKKPLDXTTEELLKMXNSTXSMXKLGAEAE-IRDIAREVLKIXGEYS 213
DB 171 ANIMLDKMOHLASEGSSCLDMFEHI-----SLMTLDSLOKCIFFSPSHCOERPSEYI 222
QY 214 LTFPIXPFLKXKLVGKYEKRIDIDLKFP-----PVERVYIKKRX 253
DB 223 AT--LLELSAL---VEKRSQHILQHMDFLYLHSDGRFRHRCRLVHDFDAVIRERR 276
QY 254 IYRRXNGEXXGEXSGVXLD--TLLEPADETXEIKTKXXIXGLVVDXFSAGXDSTAX 311
DB 277 TLPFGIDDFKDKAKSKTLDIFDIVLLSKDBDGK-ALSDEDIIRADPTFMFGHDTTAS 335
QY 312 XTEWALAEIINNXYLXAXREXYSVVGKDXLVDEV---DTQNLPIRAIVKETFRMHP 368
DB 336 GLSWVLVNLARHPEYQERCRQEVQELL-KDRDPKEIEMWDLAQLPFLTWCVESIRLHP 394
QY 369 LPVVRKCKXEECKI-NGVXVPEGALXKFNWQVGDXXKYMDRPSXRPRLFETAAEGEA 427
DB 395 APFISRCTQDVLVLPDGRVTPKGITCLIDIIGVHNPTWMPDEYVDPFRFPENSKGS 454
QY 428 XLLDLRGXHFQLLPFGSGRXPMPGVXLTATSGXATLLASLIQCF 470
DB 455 -----PLAFIPPSAGPRNCIGQAFAMAEMKVIALMLLHF 489

Search completed: December 22, 2005, 00:16:06
Job time : 46 secs

```


GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using BW model

Run on: December 21, 2005, 23:57:55 ; Search time 114 Seconds
(without alignments)
1909.553 Million cell updates/sec

Title: US-09-857-581b-66

Perfect score: 2389

Sequence: 1 MLEIALGLXVIALFXHLRP.....ASHVCPVLRIGVASKILLS 521

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:*

- 1: /cgn2_6/prodata/1/pubppaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/prodata/1/pubppaa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/prodata/1/pubppaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/prodata/1/pubppaa/US10a_PUBCOMB.pep:*
- 5: /cgn2_6/prodata/1/pubppaa/US10b_PUBCOMB.pep:*
- 6: /cgn2_6/prodata/1/pubppaa/US11_PUBCOMB.pep:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|---------------------|-------------------|
| 1 | 2259 | 94.6 | 521 | US-10-732-923-24073 | Sequence 24073, A |
| 2 | 2257 | 94.5 | 521 | US-10-732-923-1112 | Sequence 1112, Ap |
| 3 | 2257 | 94.5 | 521 | US-10-732-923-24055 | Sequence 24055, A |
| 4 | 2257 | 94.5 | 521 | US-10-732-923-24054 | Sequence 24054, A |
| 5 | 2257 | 94.5 | 521 | US-10-732-923-735 | Sequence 735, App |
| 6 | 2256 | 94.4 | 521 | US-10-732-923-648 | Sequence 648, App |
| 7 | 2256 | 94.4 | 521 | US-10-732-923-24056 | Sequence 24056, A |
| 8 | 2256 | 94.4 | 521 | US-10-659-755-2 | Sequence 2, Appl1 |
| 9 | 2250 | 94.2 | 521 | US-10-505-145-4 | Sequence 4, Appl1 |
| 10 | 2248 | 94.1 | 500 | US-10-732-923-1100 | Sequence 1100, Ap |
| 11 | 2178 | 91.2 | 500 | US-10-732-923-1102 | Sequence 1102, Ap |
| 12 | 2175 | 91.0 | 500 | US-10-732-923-1103 | Sequence 1103, Ap |
| 13 | 2174 | 91.0 | 500 | US-10-732-923-1101 | Sequence 1101, Ap |
| 14 | 2173 | 91.0 | 500 | US-10-732-923-24071 | Sequence 24071, A |
| 15 | 2173 | 91.0 | 500 | US-10-732-923-1082 | Sequence 1082, Ap |
| 16 | 2172 | 90.9 | 500 | US-10-732-923-1099 | Sequence 1099, Ap |
| 17 | 2172 | 90.9 | 500 | US-10-732-923-24070 | Sequence 24070, A |
| 18 | 2172 | 90.9 | 500 | US-10-732-923-1105 | Sequence 1105, Ap |
| 19 | 2171 | 90.9 | 500 | US-10-732-923-1104 | Sequence 1104, Ap |
| 20 | 2169 | 90.8 | 499 | US-10-732-923-1083 | Sequence 1083, Ap |
| 21 | 2163 | 90.5 | 521 | US-10-732-923-24074 | Sequence 24074, A |
| 22 | 2140 | 89.6 | 511 | US-10-739-930-9041 | Sequence 9041, Ap |
| 23 | 2130 | 89.2 | 523 | US-10-732-923-24088 | Sequence 24088, A |
| 24 | 1969.5 | 82.4 | 525 | US-10-732-923-24069 | Sequence 24069, A |
| 25 | 1946 | 80.3 | 523 | US-10-732-923-24072 | Sequence 24072, A |
| 26 | 1918 | 81.5 | 518 | US-10-732-923-1086 | Sequence 1086, Ap |
| 27 | 1896 | 79.4 | 518 | US-10-732-923-1086 | Sequence 1086, Ap |

| | | | | | |
|----|-------|------|-----|----------------------|--------------------|
| 28 | 1216 | 50.9 | 523 | US-10-732-923-24089 | Sequence 24089, A |
| 29 | 1212 | 50.7 | 523 | US-10-732-923-24090 | Sequence 24090, A |
| 30 | 944.5 | 39.5 | 512 | US-10-411-115-4 | Sequence 4, Appl1 |
| 31 | 944.5 | 39.5 | 512 | US-10-411-115-4 | Sequence 4, Appl1 |
| 32 | 940.5 | 39.4 | 506 | US-10-411-115-2 | Sequence 2, Appl1 |
| 33 | 940.5 | 39.4 | 506 | US-10-411-115-2 | Sequence 2, Appl1 |
| 34 | 940.5 | 39.4 | 506 | US-10-732-923-1107 | Sequence 1107, Ap |
| 35 | 932.5 | 39.0 | 511 | US-10-732-923-1084 | Sequence 1084, Ap |
| 36 | 921.5 | 38.6 | 506 | US-10-411-115-8 | Sequence 8, Appl1 |
| 37 | 921.5 | 38.6 | 506 | US-10-411-115-8 | Sequence 8, Appl1 |
| 38 | 919.5 | 38.5 | 509 | US-10-424-599-149724 | Sequence 149724, A |
| 39 | 891.5 | 37.3 | 509 | US-10-424-599-221409 | Sequence 221409, A |
| 40 | 870 | 36.4 | 510 | US-10-424-599-263430 | Sequence 263430, A |
| 41 | 843 | 35.3 | 502 | US-10-437-963-150757 | Sequence 150757, A |
| 42 | 807.5 | 33.8 | 579 | US-10-437-963-150757 | Sequence 150757, A |
| 43 | 761.5 | 31.9 | 518 | US-10-437-963-123495 | Sequence 123495, A |
| 44 | 753.5 | 31.5 | 518 | US-10-732-923-24084 | Sequence 24084, A |
| 45 | 730.5 | 30.6 | 516 | US-10-437-963-169616 | Sequence 169616, A |

ALIGNMENTS

| | | |
|-----------------------|--|---------------------------------------|
| RESULT 1 | US-10-732-923-24073 | Application US/10732923 |
| / | Sequence 24073, Appl1 | US/10732923 |
| / | Publication No. US20050108791A1 | |
| / | GENERAL INFORMATION: | |
| / | APPLICANT: Edgerton, Michael D | |
| / | TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES | |
| / | FILE REFERENCE: 38-15(52786)C | |
| / | CURRENT FILING DATE: 2003-12-10 | |
| / | PRIOR APPLICATION NUMBER: 10/310,154 | |
| / | PRIOR FILING DATE: 2002-12-04 | |
| / | NUMBER OF SEQ ID NOS: 24149 | |
| / | SEQ ID NO 24073 | |
| / | LENGTH: 521 | |
| / | TYPE: PRT | |
| / | ORGANISM: Pisum sativum | |
| / | US-10-732-923-24073 | |
| Query Match | 94.6% | Score 2259; DB 5; Length 521; |
| Best Local Similarity | 86.8% | Pred. No. 3,9e-256; Indels 0; Gaps 0; |
| Matches | 452; Conservative | 0; Mismatches 69; Indels 0; Gaps 0; |
| QY | 1 MLEIALGLXVIALFXHLRPFPXAKSKALRHPNPPSPXPLPFGHXLKDKLHYAX 60 | |
| DB | 1 MLEIALGLFVIALFLHLRFPSPAKSKALRHPNPPSPXPLPFGHXLKDKLHYAL 60 | |
| QY | 61 IDLSKKGHGFPSXFGSMPTVASTPELFLQXXEATSEYTRPQTSAXRYLYDXVA 120 | |
| DB | 61 IDLSKKGHGFPSXFGSMPTVASTPELFLQXXEATSEYTRPQTSAXRYLYDXVA 120 | |
| QY | 121 KXPXGPFYKFKLIMNDLXNATTTNKLRLPTQOIRKLRMAQXAEKXRLDXTBEL 180 | |
| DB | 121 KXPXGPFYKFKLIMNDLXNATTTNKLRLPTQOIRKLRMAQXAEKXRLDXTBEL 180 | |
| QY | 181 KXNKGTXSMXKGEABEIRDIAREVLKIXGSLTDFIXPLKLYGKYEKIDIDLNKF 240 | |
| DB | 181 KXNKGTXSMXKGEABEIRDIAREVLKIXGSLTDFIXPLKLYGKYEKIDIDLNKF 240 | |
| QY | 241 DVEVERVIKKRRXIVRRXNGEXXGEXSGVLDLLEFADDTYKIKTKXXIXGLVVD 300 | |
| DB | 241 DVEVERVIKKRRXIVRRXNGEXXGEXSGVLDLLEFADDTYKIKTKXXIXGLVVD 300 | |
| QY | 301 XNSAGDSTAXXTWALAEINNPLYLXAREEXSVGKDLVBDQNLPTIRAYK 360 | |
| DB | 301 XNSAGDSTAXXTWALAEINNPLYLXAREEXSVGKDLVBDQNLPTIRAYK 360 | |
| QY | 361 EFRPMPLPYVYKCKEEXKNGKXPEGALXXFNWQVGDXXKXWDPSEKXPERFLE 420 | |
| DB | 361 EFRPMPLPYVYKCKEEXKNGKXPEGALXXFNWQVGDXXKXWDPSEKXPERFLE 420 | |

QY 421 TXAEGAXXLDLRGXHFOLLPGSGRXXMCPGVXLATSGXATLLASLIQCFDLQVLGPQGO 480
 DB 421 TGAEBEAPLDLRGQHFOLLPGSGRXXMCPGVNLATSGATLLASLIQCFDLQVLGPQGO 480
 QY 481 ILKGDADAVSMERAGLTVPRAHSLVCVPLARIGVASKILLS 521
 DB 481 ILKGDADAVSMERAGLTVPRAHSLVCVPLARIGVASKILLS 521

RESULT 2

US-10-732-923-1112
 ; Sequence 1112, Application US/10732923
 ; Publication No. US20050108791A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Edgerton, Michael D
 ; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
 ; FILE REFERENCE: 38-15(52796)C
 ; CURRENT APPLICATION NUMBER: US/10/732,923
 ; CURRENT FILING DATE: 2003-12-10
 ; PRIOR APPLICATION NUMBER: 10/310,154
 ; PRIOR FILING DATE: 2002-12-04
 ; NUMBER OF SEQ ID NOS: 24149
 ; SEQ ID NO 1112
 ; LENGTH: 521
 ; TYPE: PRT
 ; ORGANISM: Trifolium pratense
 US-10-732-923-1112

Query Match 94.5%; Score 2257; DB 5; Length 521;
 Best Local Similarity 86.8%; Pred. No. 6.7e-256;
 Matches 452; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 1 MLELALGLXVLALEFXHLRPTPAXSKALRHLNPPSPKRLPTIGHXHLKDKLLHYAX 60
 DB 1 MLELALGLVLALEFXHLRPTPAXSKALRHLNPPSPKRLPTIGHXHLKDKLLHYAL 60
 QY 61 IDLSKKGFLFSXXFGSMPTVASTPELFKLFLOXXEATSFYTRFOTSAXKXLYDXVYA 120
 DB 61 IDLSKKGFLFSLYFGSMPTVASTPELFKLFLOTHEATSFYTRFOTSARLTYDSSVA 120
 QY 121 XXPGPYMKFVRKLIIMNDLNAATVNNKRLPRTQOIRKXLRXMAQXAKPDLTTELL 180
 DB 121 WPIPIPYMKFVRKLIIMNDLNAATVNNKRLPRTQOIRKXLRXMAQXAKPDLTTELL 180
 QY 181 KXNSTXSMKLGAEBEIRDIAREVLKIXGEYSLDFIXPLKXKVGKXERIDIDLNKF 240
 DB 181 KXNSTXSMKLGAEBEIRDIAREVLKIXGEYSLDFIXPLKXKVGKXERIDIDLNKF 240
 QY 241 DPVERVIRKRRXIVRRRNGEXXEGEXGVXLDTLLEFADETXEIKITKXXIXGLVVD 300
 DB 241 DPVERVIRKRRXIVRRRNGEXXEGEXGVXLDTLLEFADETXEIKITKXXIXGLVVD 300
 QY 301 XFSAGXDSSTAXXTMALAEILNNPVLYXAREEYXSVGKRLVDEVTQNLPTIRATVK 360
 DB 301 XFSAGXDSSTAXXTMALAEILNNPVLYXAREEYXSVGKRLVDEVTQNLPTIRATVK 360
 QY 361 EFRHNPPLPVYKRCXBECKXINGVXPEGALXXFNWQVGDXXKWPSPSEXPREFLE 420
 DB 361 EFRHNPPLPVYKRCXBECKXINGVXPEGALXXFNWQVGDXXKWPSPSEXPREFLE 420
 QY 421 TXAEGAXXLDLRGXHFOLLPGSGRXXMCPGVXLATSGXATLLASLIQCFDLQVLGPQGO 480
 DB 421 TGAEBEAPLDLRGQHFOLLPGSGRXXMCPGVNLATSGATLLASLIQCFDLQVLGPQGO 480
 QY 481 ILKGDADAVSMERAGLTVPRAHSLVCVPLARIGVASKILLS 521
 DB 481 ILKGDADAVSMERAGLTVPRAHSLVCVPLARIGVASKILLS 521

RESULT 3

US-10-732-923-24055
 ; Sequence 24055, Application US/10732923

; Publication No. US20050108791A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Edgerton, Michael D
 ; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
 ; FILE REFERENCE: 38-15(52796)C
 ; CURRENT APPLICATION NUMBER: US/10/732,923
 ; CURRENT FILING DATE: 2003-12-10
 ; PRIOR APPLICATION NUMBER: 10/310,154
 ; PRIOR FILING DATE: 2002-12-04
 ; NUMBER OF SEQ ID NOS: 24149
 ; SEQ ID NO 24055
 ; LENGTH: 521
 ; TYPE: PRT
 ; ORGANISM: Vigna radiata
 US-10-732-923-24055

Query Match 94.5%; Score 2257; DB 5; Length 521;
 Best Local Similarity 86.8%; Pred. No. 6.7e-256;
 Matches 452; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 1 MLELALGLXVLALEFXHLRPTPAXSKALRHLNPPSPKRLPTIGHXHLKDKLLHYAX 60
 DB 1 MLELALGLVLALEFXHLRPTPAXSKALRHLNPPSPKRLPTIGHXHLKDKLLHYAL 60
 QY 61 IDLSKKGFLFSXXFGSMPTVASTPELFKLFLOXXEATSFYTRFOTSAXKXLYDXVYA 120
 DB 61 IDLSKKGFLFSLYFGSMPTVASTPELFKLFLOTHEATSFYTRFOTSARLTYDSSVA 120
 QY 121 XXPGPYMKFVRKLIIMNDLNAATVNNKRLPRTQOIRKXLRXMAQXAKPDLTTELL 180
 DB 121 WPIPIPYMKFVRKLIIMNDLNAATVNNKRLPRTQOIRKXLRXMAQXAKPDLTTELL 180
 QY 181 KXNSTXSMKLGAEBEIRDIAREVLKIXGEYSLDFIXPLKXKVGKXERIDIDLNKF 240
 DB 181 KXNSTXSMKLGAEBEIRDIAREVLKIXGEYSLDFIXPLKXKVGKXERIDIDLNKF 240
 QY 241 DPVERVIRKRRXIVRRRNGEXXEGEXGVXLDTLLEFADETXEIKITKXXIXGLVVD 300
 DB 241 DPVERVIRKRRXIVRRRNGEXXEGEXGVXLDTLLEFADETXEIKITKXXIXGLVVD 300
 QY 301 XFSAGXDSSTAXXTMALAEILNNPVLYXAREEYXSVGKRLVDEVTQNLPTIRATVK 360
 DB 301 XFSAGXDSSTAXXTMALAEILNNPVLYXAREEYXSVGKRLVDEVTQNLPTIRATVK 360
 QY 361 EFRHNPPLPVYKRCXBECKXINGVXPEGALXXFNWQVGDXXKWPSPSEXPREFLE 420
 DB 361 EFRHNPPLPVYKRCXBECKXINGVXPEGALXXFNWQVGDXXKWPSPSEXPREFLE 420
 QY 421 TXAEGAXXLDLRGXHFOLLPGSGRXXMCPGVXLATSGXATLLASLIQCFDLQVLGPQGO 480
 DB 421 TGAEBEAPLDLRGQHFOLLPGSGRXXMCPGVNLATSGATLLASLIQCFDLQVLGPQGO 480
 QY 481 ILKGDADAVSMERAGLTVPRAHSLVCVPLARIGVASKILLS 521
 DB 481 ILKGDADAVSMERAGLTVPRAHSLVCVPLARIGVASKILLS 521

RESULT 4

US-10-732-923-24057
 ; Sequence 24057, Application US/10732923
 ; Publication No. US20050108791A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Edgerton, Michael D
 ; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
 ; FILE REFERENCE: 38-15(52796)C
 ; CURRENT APPLICATION NUMBER: US/10/732,923
 ; CURRENT FILING DATE: 2003-12-10
 ; PRIOR APPLICATION NUMBER: 10/310,154
 ; PRIOR FILING DATE: 2002-12-04
 ; NUMBER OF SEQ ID NOS: 24149
 ; SEQ ID NO 24057
 ; LENGTH: 521
 ; TYPE: PRT

ORGANISM: Vigna radiata
US-10-732-923-24057

Query Match 94.5%; Score 2257; DB 5; Length 521;
Best Local Similarity 86.8%; Pred. No. 6.7e-256;
Matches 452; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

```

QY 1 MLELALGLXVLALEFXHLRPTPXAXSKALRHLNPNPSPXPRLPFIQXHLKDKLLHYAX 60
DB 1 MLELALGLVLALEFLHRLPTPTAKSKALRHLNPNPSPXPRLPFIQHLHLKDKLLHYAL 60
QY 61 IDLSKHGRLPSXFGSMPTVASTPELFLQXXEATSEKTRQTSAXRLTYDSSVA 120
DB 61 IDLSKHGRLPSLFGSMPTVASTPELFLQTHEATSEKTRQTSARLTLYDSSVA 120
QY 121 XXXPAPYKFPVKLIIMNDLXNATTVNKLRLPTQOIRKFLRMAQGAQKPLDTELL 180
DB 121 XXXPAPYKFPVKLIIMNDLXNATTVNKLRLPTQOIRKFLRMAQGAQKPLDTELL 180
QY 121 MVPFGRPYMKFKLIMNDLXNATTVNKLRLPTQOIRKFLRMAQGAQKPLDTELL 180
DB 121 MVPFGRPYMKFKLIMNDLXNATTVNKLRLPTQOIRKFLRMAQGAQKPLDTELL 180
QY 181 KXNSTXSMXKLGAEBEIRDIAREVLKIXGEYSLTDFIXPLKXKLVGKYEKIDILNKF 240
DB 181 KXNSTXSMXKLGAEBEIRDIAREVLKIXGEYSLTDFIXPLKXKLVGKYEKIDILNKF 240
QY 181 KXNSTXSMXKLGAEBEIRDIAREVLKIXGEYSLTDFIXPLKXKLVGKYEKIDILNKF 240
DB 181 KXNSTXSMXKLGAEBEIRDIAREVLKIXGEYSLTDFIXPLKXKLVGKYEKIDILNKF 240
QY 241 DPEVERVIKRRXIVRRXNXXGEXSGVXLDTLLEFADETXEIKITKXXIXGLVVD 300
DB 241 DPEVERVIKRRXIVRRXNXXGEXSGVXLDTLLEFADETXEIKITKXXIXGLVVD 300
QY 301 XFSAGXSTAXXTWALAEILINNPVYLXXAREEYXSVGKDLVDEVTQMLPYIRAYK 360
DB 301 XFSAGXSTAXXTWALAEILINNPVYLXXAREEYXSVGKDLVDEVTQMLPYIRAYK 360
QY 301 XFSAGXSTAXXTWALAEILINNPVYLXXAREEYXSVGKDLVDEVTQMLPYIRAYK 360
DB 301 XFSAGXSTAXXTWALAEILINNPVYLXXAREEYXSVGKDLVDEVTQMLPYIRAYK 360
QY 361 EFPFMRHPLPVYKRCCKEEXINGXVYPEGALXXFNWQVGDXXKWDPSXPERPLE 420
DB 361 EFPFMRHPLPVYKRCCKEEXINGXVYPEGALXXFNWQVGDXXKWDPSXPERPLE 420
QY 421 TYAEGEAXXLDLRGXHFOLLFPGSGRMCPCGYXLATSGXATLLASLIQCFDLQVLGPQO 480
DB 421 TYAEGEAXXLDLRGXHFOLLFPGSGRMCPCGYXLATSGXATLLASLIQCFDLQVLGPQO 480
QY 481 ILKGDARVSMERAGLTVPRASHIVCVPLARIGVASKILLS 521
DB 481 ILKGDARVSMERAGLTVPRASHIVCVPLARIGVASKILLS 521

```

RESULT 5

US-10-732-923-24054
Sequence 24054, Application US/10732923
Publication No. US20050108791A1
GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REFERENCE: 38-15(52796)C
CURRENT APPLICATION NUMBER: US/10/732,923
CURRENT FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: 10/310,154
PRIOR FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 24149
SEQ ID NO 24054
LENGTH: 522
TYPE: PRT
ORGANISM: Vigna radiata
US-10-732-923-24054

Query Match 94.5%; Score 2257; DB 5; Length 521;
Best Local Similarity 86.8%; Pred. No. 6.7e-256;
Matches 452; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

```

QY 1 MLELALGLXVLALEFXHLRPTPXAXSKALRHLNPNPSPXPRLPFIQXHLKDKLLHYAX 60
DB 1 MLELALGLVLALEFLHRLPTPTAKSKALRHLNPNPSPXPRLPFIQHLHLKDKLLHYAL 60
QY 61 IDLSKHGRLPSXFGSMPTVASTPELFLQXXEATSEKTRQTSAXRLTYDSSVA 120
DB 61 IDLSKHGRLPSLFGSMPTVASTPELFLQTHEATSEKTRQTSARLTLYDSSVA 120

```

```

DB 61 IDLSKHGRLPSLFGSMPTVASTPELFLQTHEATSEKTRQTSARLTLYDSSVA 120
QY 121 XXXPAPYKFPVKLIIMNDLXNATTVNKLRLPTQOIRKFLRMAQGAQKPLDTELL 180
DB 121 MVPFGRPYMKFKLIMNDLXNATTVNKLRLPTQOIRKFLRMAQGAQKPLDTELL 180
QY 181 KXNSTXSMXKLGAEBEIRDIAREVLKIXGEYSLTDFIXPLKXKLVGKYEKIDILNKF 240
DB 181 KXNSTXSMXKLGAEBEIRDIAREVLKIXGEYSLTDFIXPLKXKLVGKYEKIDILNKF 240
QY 241 DPEVERVIKRRXIVRRXNXXGEXSGVXLDTLLEFADETXEIKITKXXIXGLVVD 300
DB 241 DPEVERVIKRRXIVRRXNXXGEXSGVXLDTLLEFADETXEIKITKXXIXGLVVD 300
QY 301 XFSAGXSTAXXTWALAEILINNPVYLXXAREEYXSVGKDLVDEVTQMLPYIRAYK 360
DB 301 XFSAGXSTAXXTWALAEILINNPVYLXXAREEYXSVGKDLVDEVTQMLPYIRAYK 360
QY 361 EFPFMRHPLPVYKRCCKEEXINGXVYPEGALXXFNWQVGDXXKWDPSXPERPLE 420
DB 361 EFPFMRHPLPVYKRCCKEEXINGXVYPEGALXXFNWQVGDXXKWDPSXPERPLE 420
QY 421 TYAEGEAXXLDLRGXHFOLLFPGSGRMCPCGYXLATSGXATLLASLIQCFDLQVLGPQO 480
DB 421 TYAEGEAXXLDLRGXHFOLLFPGSGRMCPCGYXLATSGXATLLASLIQCFDLQVLGPQO 480
QY 481 ILKGDARVSMERAGLTVPRASHIVCVPLARIGVASKILLS 521
DB 481 ILKGDARVSMERAGLTVPRASHIVCVPLARIGVASKILLS 521

```

RESULT 6

US-10-310-154-735
Sequence 735, Application US/10310154
Publication No. US2003023670A1

GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
APPLICANT: Chomet, Paul S.
APPLICANT: Adams, Thomas H.
APPLICANT: Ruff, Thomas G.
APPLICANT: Agarwal, Ameeta K.
APPLICANT: Ahrens, Jeffrey E.
APPLICANT: Ball, James A.
APPLICANT: Banu, G.
APPLICANT: Bell, Erin
APPLICANT: Boddupalli, Raghava
APPLICANT: Deikman, Jill
APPLICANT: Deng, Molian
APPLICANT: Dong, Jinzuo
APPLICANT: Duff, Stephen M.
APPLICANT: Galligan, Meghan M.
APPLICANT: Hinchey, Brenda S.
APPLICANT: Huang, Shishieh
APPLICANT: Johnson, G. Richard
APPLICANT: Jung, Vincent
APPLICANT: Kretzmer, Keith A.
APPLICANT: Laccetti, Lucille B.
APPLICANT: Lai, Chao-Qiang
APPLICANT: Lee, Gary
APPLICANT: Lin, Jie-Yi
APPLICANT: Liu, Jindong
APPLICANT: Lu, Bin
APPLICANT: Luethy, Michael M.
APPLICANT: Madison, Linda L.
APPLICANT: Malloy, Kathleen A.
APPLICANT: McKiel, Christine L.
APPLICANT: Miller, Philip W.
APPLICANT: Padmavathi, Manchi Kant
APPLICANT: Parnell, Laurence D.
APPLICANT: Start, William G.
APPLICANT: Tennesen, Dan
APPLICANT: Vidya, K.R.

APPLICANT: Wang, Haiyun
APPLICANT: Xin, zhanguo
APPLICANT: Xu, Nanfei
APPLICANT: Yang, Chunzhi
APPLICANT: Zeng, Xiaoping
APPLICANT: Zhang, Qiang
APPLICANT: Zhao, Yajuan
APPLICANT: Zhou, Li
TITLE OF INVENTION: Gene Sequences and Uses Thereof in Plants
FILE REFERENCE: 38-15(52796)B
CURRENT APPLICATION NUMBER: US/10/310,154
PRIOR FILING DATE: 2002-12-04
PRIOR APPLICATION NUMBER: 60/337,358
NUMBER OF SEQ ID NOS: 736
SEQ ID NO 735
LENGTH: 521
TYPE: PRT
ORGANISM: Glycine max
US-10-310-154-735

Query Match 94.4%; Score 2256; DB 4; Length 521;
Best Local Similarity 86.8%; Pred. No. 8.8e-256;
Matches 452; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 1 MLELALGLXVALFXHLRPTPXASKALRHLPNPSPXPRLPFIQHXHLKDKLHYAX 60
DB 1 MLELALGLXVALFXHLRPTPXASKALRHLPNPSPXPRLPFIQHXHLKDKLHYAX 60
QY 61 IDLSKKGPLFSXXFGSMPTVASTPELFKFLQXXEATSPYTRFQTSAXKXLYDXVA 120
DB 61 IDLSKKGPLFSXXFGSMPTVASTPELFKFLQXXEATSPYTRFQTSAXKXLYDXVA 120
QY 121 XXPXGPYKXFKRLIMNDLXNATTVNKLRLPTQOIRKCLRMAQXABKPLDXTBEL 180
DB 121 XXPXGPYKXFKRLIMNDLXNATTVNKLRLPTQOIRKCLRMAQXABKPLDXTBEL 180
QY 121 MFPGPYKXFKRLIMNDLXNATTVNKLRLPTQOIRKCLRMAQXABKPLDXTBEL 180
DB 121 MFPGPYKXFKRLIMNDLXNATTVNKLRLPTQOIRKCLRMAQXABKPLDXTBEL 180
QY 181 KMXNSTXSMXKLGEABEIRDIAREVLKIXGEYSITDFIXPLKXKVKYKXKIDILNKF 240
DB 181 KMXNSTXSMXKLGEABEIRDIAREVLKIXGEYSITDFIXPLKXKVKYKXKIDILNKF 240
QY 241 DTVVERVVKRRXIVRRXNGEXXGEXSGVXLDTLLEFADETXEIKITKXXIXGLVVD 300
DB 241 DTVVERVVKRRXIVRRXNGEXXGEXSGVXLDTLLEFADETXEIKITKXXIXGLVVD 300
QY 241 DTVVERVVKRRXIVRRXNGEXXGEXSGVXLDTLLEFADETXEIKITKXXIXGLVVD 300
DB 241 DTVVERVVKRRXIVRRXNGEXXGEXSGVXLDTLLEFADETXEIKITKXXIXGLVVD 300
QY 301 XFSAGDSTAXXTMALAEILNNPVVLXAREEYSVVGKRLVDEVDTONLPYIRATVK 360
DB 301 XFSAGDSTAXXTMALAEILNNPVVLXAREEYSVVGKRLVDEVDTONLPYIRATVK 360
QY 361 ETRFMHPLPVVKRCXECXINGVXPEGALXFNVMQVGDXXKXWDRPSEXPREFLE 420
DB 361 ETRFMHPLPVVKRCXECXINGVXPEGALXFNVMQVGDXXKXWDRPSEXPREFLE 420
QY 421 TXAGEAXXLDLRGXHPLLPGSGRXXMCPGVXALATSGXATLLASLIQCFDLQVLGPQG 480
DB 421 TXAGEAXXLDLRGXHPLLPGSGRXXMCPGVXALATSGXATLLASLIQCFDLQVLGPQG 480
QY 481 ILKGDADKVSMEERAGLTVPRASHLVCVPLARIGVASKLS 521
DB 481 ILKGDADKVSMEERAGLTVPRASHLVCVPLARIGVASKLS 521

RESULT 7
US-10-732-923-648
Sequence 648, Application US/10732923
Publication No. US20050108791A1
GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REFERENCE: 38-15(52796)C
CURRENT APPLICATION NUMBER: US/10/732,923
PRIOR FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: 10/310,154

PRIOR FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 24149
SEQ ID NO 648
LENGTH: 521
TYPE: PRT
ORGANISM: Glycine max
US-10-732-923-648

Query Match 94.4%; Score 2256; DB 5; Length 521;
Best Local Similarity 86.8%; Pred. No. 8.8e-256;
Matches 452; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 1 MLELALGLXVALFXHLRPTPXASKALRHLPNPSPXPRLPFIQHXHLKDKLHYAX 60
DB 1 MLELALGLXVALFXHLRPTPXASKALRHLPNPSPXPRLPFIQHXHLKDKLHYAX 60
QY 61 IDLSKKGPLFSXXFGSMPTVASTPELFKFLQXXEATSPYTRFQTSAXKXLYDXVA 120
DB 61 IDLSKKGPLFSXXFGSMPTVASTPELFKFLQXXEATSPYTRFQTSAXKXLYDXVA 120
QY 121 XXPXGPYKXFKRLIMNDLXNATTVNKLRLPTQOIRKCLRMAQXABKPLDXTBEL 180
DB 121 XXPXGPYKXFKRLIMNDLXNATTVNKLRLPTQOIRKCLRMAQXABKPLDXTBEL 180
QY 121 MFPGPYKXFKRLIMNDLXNATTVNKLRLPTQOIRKCLRMAQXABKPLDXTBEL 180
DB 121 MFPGPYKXFKRLIMNDLXNATTVNKLRLPTQOIRKCLRMAQXABKPLDXTBEL 180
QY 181 KMXNSTXSMXKLGEABEIRDIAREVLKIXGEYSITDFIXPLKXKVKYKXKIDILNKF 240
DB 181 KMXNSTXSMXKLGEABEIRDIAREVLKIXGEYSITDFIXPLKXKVKYKXKIDILNKF 240
QY 241 DTVVERVVKRRXIVRRXNGEXXGEXSGVXLDTLLEFADETXEIKITKXXIXGLVVD 300
DB 241 DTVVERVVKRRXIVRRXNGEXXGEXSGVXLDTLLEFADETXEIKITKXXIXGLVVD 300
QY 301 XFSAGDSTAXXTMALAEILNNPVVLXAREEYSVVGKRLVDEVDTONLPYIRATVK 360
DB 301 XFSAGDSTAXXTMALAEILNNPVVLXAREEYSVVGKRLVDEVDTONLPYIRATVK 360
QY 361 ETRFMHPLPVVKRCXECXINGVXPEGALXFNVMQVGDXXKXWDRPSEXPREFLE 420
DB 361 ETRFMHPLPVVKRCXECXINGVXPEGALXFNVMQVGDXXKXWDRPSEXPREFLE 420
QY 421 TXAGEAXXLDLRGXHPLLPGSGRXXMCPGVXALATSGXATLLASLIQCFDLQVLGPQG 480
DB 421 TXAGEAXXLDLRGXHPLLPGSGRXXMCPGVXALATSGXATLLASLIQCFDLQVLGPQG 480
QY 481 ILKGDADKVSMEERAGLTVPRASHLVCVPLARIGVASKLS 521
DB 481 ILKGDADKVSMEERAGLTVPRASHLVCVPLARIGVASKLS 521

RESULT 8
US-10-732-923-24056
Sequence 24056, Application US/10732923
Publication No. US20050108791A1
GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REFERENCE: 38-15(52796)C
CURRENT APPLICATION NUMBER: US/10/732,923
PRIOR FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: 10/310,154
NUMBER OF SEQ ID NOS: 24149
SEQ ID NO 24056
LENGTH: 521
TYPE: PRT
ORGANISM: Vigna radiata
US-10-732-923-24056

Query Match 94.4%; Score 2256; DB 5; Length 521;
Best Local Similarity 86.8%; Pred. No. 8.8e-256;
Matches 452; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 1 MLELALGLXVALFXHLRPTPXASKALRHLPNPSPXPRLPFIQHXHLKDKLHYAX 60

```

Db      1 MLELALGLVIALFLHLRPTAKSKALRHLNPPSPKPRLPFIQHLHLKDLKLAHYAL 60
Qy      61 IDLSKRGPLPSXXGSMPTVASTPELFLKLOXXEATSEKTRPOTSAKRLTYDXVA 120
Db      61 IDLSKRGPLPSLYGSMPTVASTPELFLKLOTHEATSEKTRPOTSAIRRLTYDSSVA 120
Qy      121 XXPGPYMKFVRKLIIMNDLNATTVNKLRLPTQOIRKCLRMAOXAEXAKPLDYTEELL 180
Db      121 MWPFGPYMKFVRKLIIMNDLNATTVNKLRLPTQOIRKCLRMAOXAEXAKPLDYTEELL 180
Qy      181 KMNSTXSMWMLGEABEIRDIAREVLKIXGEYSLTDFIXPLKLVKGYEKRIDILNKF 240
Db      181 KMNSTISMMWMLGEABEIRDIAREVLKIFGEYSLTDFIWPPLKLVKGYEKRIDILNKF 240
Qy      241 DPVERVVKRRKXIVRRKNGEXXGEGXGVLDLTLEFADETEIKITKXXIXGLVVD 300
Db      241 DPVERVVKRRREIYRRRNGEVEGVSGLDLEFADETEIKITKXXIXGLVVD 300
Qy      301 XPSAGDSTAXXTWMAELINNPNVIXXAREEYXSVGKDLVDEVDTONLPYIRAIYK 360
Db      301 FFSAGTDSIAATEMALBELINNPNVLEKAREEYXSVGKDLVDEVDTONLPYIRAIYK 360
Qy      361 EFRMHPLPVYKRCXECXINGVXPEGALXXFNWQVGDXYMDRPSKPERPLE 420
Db      361 EFRMHPLPVYKRCXECXINGVYIPGALILFNWQVGRDPKYMDRPSKPERPLE 420
Qy      421 TYAEGAXXLDLRGHHFOLLPPSGGRMCPGVXLATSGATLASLIQCFDLQVLGPQO 480
Db      421 TGAEGAGPLDLRGHFLPFGSGGRMCPGVNLATSGAVTLASLIQCFDLQVLGPQO 480
Qy      481 ILKGDVAVSMERAGLTVPRASHLVCPPLARIGVASKILLS 521
Db      481 ILKGDVAVSMERAGLTVPRASHLVCPPLARIGVASKILLS 521

```

```

RESULT 9
US-10-659-755-2
; Sequence 2, Application US/10659755
; Publication No. US20040128711A1
; GENERAL INFORMATION:
; APPLICANT: DIXON, RICHARD A.
; APPLICANT: LIU, CHANG-JUN
; APPLICANT: DEAVOURS, BETTINA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PRODUCTION OF FLAVONOID
; TITLE OF INVENTION: AND ISOFLAVONOID NUTRACEUTICALS
; FILE REFERENCE: NMLE:007US
; CURRENT APPLICATION NUMBER: US/10/659,755
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/409,447
; PRIOR FILING DATE: 2002-09-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentln Ver. 2.1
; LENGTH: 521
; TYPE: PRT
; ORGANISM: Soybean
US-10-659-755-2

```

```

Query Match      94.2%; Score 2250; DB 4; Length 521;
Best Local Similarity 86.6%; Pred. No. 4,4e-255;
Matches 451; Conservative 0; Mismatches 70; Indels 0; Gaps 0;
Qy      1 MLELALGLVIALFLHLRPTAKSKALRHLNPPSPKPRLPFIQHLHLKDLKLAHYAX 60
Db      1 MLELALGLVIALFLHLRPTAKSKALRHLNPPSPKPRLPFIQHLHLKDLKLAHYAL 60
Qy      61 IDLSKRGPLPSXXGSMPTVASTPELFLKLOXXEATSEKTRPOTSAKRLTYDXVA 120
Db      61 IDLSKRGPLPSLYGSMPTVASTPELFLKLOTHEATSEKTRPOTSAIRRLTYDSSVA 120
Qy      121 XXPGPYMKFVRKLIIMNDLNATTVNKLRLPTQOIRKCLRMAOXAEXAKPLDYTEELL 180

```

```

Db      121 MWPFGPYMKFVRKLIIMNDLNATTVNKLRLPTQOIRKCLRMAOXAEXAKPLDYTEELL 180
Qy      181 KMNSTXSMWMLGEABEIRDIAREVLKIXGEYSLTDFIXPLKLVKGYEKRIDILNKF 240
Db      181 KMNSTISMMWMLGEABEIRDIAREVLKIFGEYSLTDFIWPPLKLVKGYEKRIDILNKF 240
Qy      241 DPVERVVKRRKXIVRRKNGEXXGEGXGVLDLTLEFADETEIKITKXXIXGLVVD 300
Db      241 DPVERVVKRRREIYRRRNGEVEGVSGLDLEFADETEIKITKXXIXGLVVD 300
Qy      301 XPSAGDSTAXXTWMAELINNPNVIXXAREEYXSVGKDLVDEVDTONLPYIRAIYK 360
Db      301 FFSAGTDSIAATEMALBELINNPNVLEKAREEYXSVGKDLVDEVDTONLPYIRAIYK 360
Qy      361 EFRMHPLPVYKRCXECXINGVXPEGALXXFNWQVGDXYMDRPSKPERPLE 420
Db      361 EFRMHPLPVYKRCXECXINGVYIPGALILFNWQVGRDPKYMDRPSKPERPLE 420
Qy      421 TYAEGAXXLDLRGHHFOLLPPSGGRMCPGVXLATSGATLASLIQCFDLQVLGPQO 480
Db      421 TGAEGAGPLDLRGHFLPFGSGGRMCPGVNLATSGAVTLASLIQCFDLQVLGPQO 480
Qy      481 ILKGDVAVSMERAGLTVPRASHLVCPPLARIGVASKILLS 521
Db      481 ILKGDVAVSMERAGLTVPRASHLVCPPLARIGVASKILLS 521

```

```

RESULT 10
US-10-505-145-4
; Sequence 4, Application US/10505145
; Publication No. US20050241014A1
; GENERAL INFORMATION:
; APPLICANT: COLLIVER, Steven Peter
; APPLICANT: DOBB, Roy Thomas
; APPLICANT: van der HILDEN, Hendrikus Theodorus Wilhelmus Maria
; TITLE OF INVENTION: PRODUCTION OF DADZEIN IN TRANSGENIC PLANTS
; FILE REFERENCE: 56159-5241
; CURRENT APPLICATION NUMBER: US/10/505,145
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: PCT/EP03/01465
; PRIOR FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: EP 02251404.6
; PRIOR FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: Patentln version 3.2
; LENGTH: 521
; TYPE: PRT
; ORGANISM: Glycine max
US-10-505-145-4

```

```

Query Match      94.1%; Score 2248; DB 5; Length 521;
Best Local Similarity 86.4%; Pred. No. 7,6e-255;
Matches 450; Conservative 1; Mismatches 70; Indels 0; Gaps 0;
Qy      1 MLELALGLVIALFLHLRPTAKSKALRHLNPPSPKPRLPFIQHLHLKDLKLAHYAX 60
Db      1 MLELALGLVIALFLHLRPTAKSKALRHLNPPSPKPRLPFIQHLHLKDLKLAHYAL 60
Qy      61 IDLSKRGPLPSXXGSMPTVASTPELFLKLOXXEATSEKTRPOTSAKRLTYDXVA 120
Db      61 IDLSKRGPLPSLYGSMPTVASTPELFLKLOTHEATSEKTRPOTSAIRRLTYDSSVA 120
Qy      121 XXPGPYMKFVRKLIIMNDLNATTVNKLRLPTQOIRKCLRMAOXAEXAKPLDYTEELL 180
Db      121 MWPFGPYMKFVRKLIIMNDLNATTVNKLRLPTQOIRKCLRMAOXAEXAKPLDYTEELL 180
Qy      181 KMNSTXSMWMLGEABEIRDIAREVLKIXGEYSLTDFIXPLKLVKGYEKRIDILNKF 240
Db      181 KMNSTISMMWMLGEABEIRDIAREVLKIFGEYSLTDFIWPPLKLVKGYEKRIDILNKF 240
Qy      241 DPVERVVKRRKXIVRRKNGEXXGEGXGVLDLTLEFADETEIKITKXXIXGLVVD 300

```

```

Db      241 DPEVVERVTKRREIVRRKNGVEVGEVFLDTLLEFADEBTWEIKTKDHIKGLVVD 300
Qy      301 XFSAGXDSAXXTXEWALAEIINNPKYLXXAREEXYSVVGKDLVDEVDTONLPYIRAIYK 360
Db      301 FFSAGTDTAVATENAELIINNPKYLEAREEVSYVGKDLVDEVDTONLPYIRAIYK 360
Qy      361 ETRFMHPPLPVVKRKCXEBXINGVYXPEGALXXFNWQVGDXXKWDPRSEKBERPLE 420
Db      361 ETRFMHPPLPVVKRKCXEBXINGVYXPEGALILFNWQVGRDPKXWDRPSSEFRBERPLE 420
Qy      421 TXAEBEAXXLDLRGNHFOILLPGSGRKMCPGYXATLTSKATILASLIQCFDLOVGPQOQ 480
Db      421 TGAEBEABQPLDRGNHFOILLPGSGRKMCPGVNLTSGMATILASLIQCFDLOVGPQOQ 480
Qy      481 ILKGDADAKSMERAGLTVPRASHLVCVPLARIIGVASKLLS 521
Db      481 ILKGDADAKSMERAGLTVPRASHLVCVPLARIIGVASKLLS 521

```

```

RESULT 11
US-10-732-923-1100
; Sequence 1100, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 1100
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Medicago sativa
US-10-732-923-1100

```

```

Query Match      91.2%; Score 2178; DB 5; Length 500;
Best Local Similarity 86.4%; Pred. No. 1,2e-246;
Matches 432; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

```

```

Qy      15 FXHLRPTXAXSKALRHLNPPSPKRLPFIQHXHLLKDKLLHYXIDLSKKHGLFSXX 74
Db      1 FLHLRPTXAKSKALRHLNPPSPKRLPFIQHLHLKDKLLHYALIDLSKKGGLFSIX 60
Qy      75 FGSMTTVAASSTPELTKLFLQXXEATSFKTRFOTSAXRKLTDXXVAXXPGPYMKFVRKL 134
Db      61 FGSMTTVAASSTPELTKLFLQTHEATSFNTRFQTSALRRLTYDSVAMAPFGPYMKFVRKL 120
Qy      135 IMNDLXNATTVNXLRLPTQOIRKCLRMAQXAEAKPLDYTELLKMXNSTXSMXKLG 194
Db      121 IMNDLXNATTVNXLRLPTQOIRKCLRMAQXAEAKPLDYTELLKMXNSTXSMXKLG 180
Qy      195 ABEIRDIAREVLKIXGEYSITDFIXPLKXKLVGKYEKRIIDILNKFDPVEBEVIKRRXI 254
Db      181 ABEIRDIAREVLKIXGEYSITDFIRPLKXKLVGKYEKRIIDILNKFDPVEBEVIKRRXI 240
Qy      255 VRRRNGEXXGEXSGVLDLTLEFADEBTWEIKTKKHIXGLVVDXFSAGDSTAXXT 314
Db      241 VRRRNGEXXGEXSGVLDLTLEFADEBTWEIKTKKHIXGLVVDXFSAGDSTAXXT 300
Qy      315 WALAEIINNPKYLXXAREEXYSVVGKDLVDEVDTONLPYIRAIYKTRFMHPPLPVVKR 374
Db      301 WALAEIINNPKYLXXAREEXYSVVGKDLVDEVDTONLPYIRAIYKTRFMHPPLPVVKR 360
Qy      375 KCXEBXINGVYXPEGALXXFNWQVGDXXKWDPRSEKBERPLETXAEBEAXXLDLRG 434
Db      361 KCTECEINGVYXPEGALILFNWQVGRDPSKXWDRPSSEFRBERPLETGAEBEABQPLDRG 420
Qy      435 XHFOLLPGSGRKMCPGYXATLTSKATILASLIQCFDLOVGPQOQILKGDADAKSMER 494
Db      421 OHFOLLPGSGRKMCPGVNLTSGMATILASLIQCFDLOVGPQOQILKGDADAKSMER 480

```

```

Qy      495 AGLTVPRASHLVCVPLARIIG 514
Db      481 AGLTVPRASHLVCVPLARIIG 500

```

```

RESULT 12
US-10-732-923-1102
; Sequence 1102, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 1102
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Medicago sativa
US-10-732-923-1102

```

```

Query Match      91.0%; Score 2175; DB 5; Length 500;
Best Local Similarity 86.4%; Pred. No. 2,8e-246;
Matches 432; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

```

```

Qy      15 FXHLRPTXAXSKALRHLNPPSPKRLPFIQHXHLLKDKLLHYXIDLSKKHGLFSXX 74
Db      1 FLHLRPTXAKSKALRHLNPPSPKRLPFIQHLHLKDKLLHYALIDLSKKGGLFSIX 60
Qy      75 FGSMTTVAASSTPELTKLFLQXXEATSFKTRFOTSAXRKLTDXXVAXXPGPYMKFVRKL 134
Db      61 FGSMTTVAASSTPELTKLFLQTHEATSFNTRFQTSALRRLTYDSVAMAPFGPYMKFVRKL 120
Qy      135 IMNDLXNATTVNXLRLPTQOIRKCLRMAQXAEAKPLDYTELLKMXNSTXSMXKLG 194
Db      121 IMNDLXNATTVNXLRLPTQOIRKCLRMAQXAEAKPLDYTELLKMXNSTXSMXKLG 180
Qy      195 ABEIRDIAREVLKIXGEYSITDFIXPLKXKLVGKYEKRIIDILNKFDPVEBEVIKRRXI 254
Db      181 ABEIRDIAREVLKIXGEYSITDFIWPVKLVGKYEKRIIDILNKFDPVEBEVIKRRXI 240
Qy      255 VRRRNGEXXGEXSGVLDLTLEFADEBTWEIKTKKHIXGLVVDXFSAGDSTAXXT 314
Db      241 VRRRNGEXXGEXSGVLDLTLEFADEBTWEIKTKKHIXGLVVDXFSAGDSTAXXT 300
Qy      315 WALAEIINNPKYLXXAREEXYSVVGKDLVDEVDTONLPYIRAIYKTRFMHPPLPVVKR 374
Db      301 WALAEIINNPKYLXXAREEXYSVVGKDLVDEVDTONLPYIRAIYKTRFMHPPLPVVKR 360
Qy      375 KCXEBXINGVYXPEGALXXFNWQVGDXXKWDPRSEKBERPLETXAEBEAXXLDLRG 434
Db      361 KCTECEINGVYXPEGALVLFNWWQVGRDPKXWDRPSSEFRBERPLETGAEBEABQPLDRG 420
Qy      435 XHFOLLPGSGRKMCPGYXATLTSKATILASLIQCFDLOVGPQOQILKGDADAKSMER 494
Db      421 OHFOLLPGSGRKMCPGVNLTSGMATILASLIQCFDLOVGPQOQILKGDADAKSMER 480
Qy      495 AGLTVPRASHLVCVPLARIIG 514
Db      481 AGLTVPRASHLVCVPLARIIG 500

```

```

RESULT 13
US-10-732-923-1103
; Sequence 1103, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES

```

```

: FILE REFERENCE: 38-15(52796)C
: CURRENT APPLICATION NUMBER: US/10/732,923
: CURRENT FILING DATE: 2003-12-10
: PRIOR APPLICATION NUMBER: 10/310,154
: PRIOR FILING DATE: 2002-12-04
: NUMBER OF SEQ ID NOS: 24149
: SEQ ID NO 1103
:
: LENGTH: 500
:
: TYPE: PRT
:
: ORGANISM: Trifolium repens
:
: US-10-732-923-1103

```

| | | | | |
|------------------------|--------------|-------------------|---------------|------------|
| Query Match Similarity | 91.0% | Score 2174 | DB 5 | length 500 |
| Best Local Similarity | 86.4% | Pred No. 3.6e-246 | | |
| Matches 432 | Conservative | 0 | Mismatches 68 | Indels 0 |
| | | | | Gaps 0 |

| | | | |
|----|-----|---|-----|
| QY | 15 | FXLHPRPYXASKALRHLPNPSPKPRPLPFIOHXLHDKLHAYXKIDLSKGGPFSKX | 74 |
| Db | 1 | FLHLRPTTASKSALRHLPNPSPKPRPLPFIOHXLHDKLHAYXKIDLSKGGPFSKX | 60 |
| QY | 75 | FGSMPTVAASPPELKFULOXXEASFSKTRPOTSAKRLTYXVAXXPGYXMFVRU | 134 |
| Db | 61 | FGSMPTVAASPPELKFULOTHEASFNTRPOTSAIRLTYNSVAMVPGFYMKFVRU | 120 |
| QY | 135 | IMNDLXNATTVXKLRPLRTOQIRKXLRKMAOAXEAKKPLDXTEEBLKWANSYXSMMKLG | 194 |
| Db | 121 | IMNDLXNATTVXKLRPLRTOQIRKRLRWAGASAEQKPLDYVEBLLKWNSITSMWMLGE | 180 |
| QY | 195 | ABEIRDIAREVLKIXGEYSLDFIXPLKXKVKGTREKRIDIDLINKFDPYVERVIKKRKXI | 254 |
| Db | 181 | ABEIRDIAREVLKIXGEYSLDFIPIPLKXKIKGKYEKRIDIDLINKFDPVERVIKKRGREI | 240 |
| QY | 255 | VRRKNGEXXEGXEGVXLDTLLEFADETTXEIKTKKXIXGLVVDXFSAGXDSFXAXTE | 314 |
| Db | 241 | VRRKNGEXVVEBASGVFLDTLLEFREDDTMEIKTKKQIKGLVVDFFSAGDSTRTVAHE | 300 |
| QY | 315 | WALAEILINNFXVXAXAREEYSVVGKDXLVEVDTONLPIRAIVKETFRMHPPLEPVKR | 374 |
| Db | 301 | WALAEILINNPKVLOXAREEAYSVGKDRLVDEVDTONLPIRAIVETFRMHPPLEPVKR | 360 |
| QY | 375 | KCXEECXINGVXPGGALXXFNVMVOGXGXKXWDRESEKRPERSPLETXXAGEAXXLDLNG | 434 |
| Db | 361 | KCTEBCGINGVYIPGALVLFVMVOGGRPKIMDRSESRPERFLETGABEGBGPJDLNG | 420 |
| QY | 435 | XHFOLLPFSGSGRMCXPGVXLATSGAXTLLASLIQCEDLVLAGOQOILKGXDAXVSEER | 494 |
| Db | 421 | QHFOILLPFSGSGRMCXGVNLATSGMATLLASLIQCEDLVLAGOQOILKGDDAKVSEER | 480 |
| QY | 495 | AGLTVPRASHLVCVPLARIG 514 | |
| Db | 481 | AGLTVPRASHLVCVPLARIG 500 | |

RESULT 14
US-10-732-923-1101

Query Match 91.0%; Score 2173; DB 5; Length 500,

```
Best Local Similarity 86.4%; Pred. No. 4.8e-246;
Matches 432; Conservative 0; Mismatches 68; Indels 0; Gaps 0;
```

| | | | |
|----|-----|---|-----|
| QY | 15 | FYHLRPLRPMXKSKLRLHPNDPSPRLPFGXHLKDKLXHLXIDLSSKHGGLFSFX | 74 |
| Db | 1 | FLHLRPLRPMXKSKLRLHPNDPSPKRLPFGHLHLKDKLXHLXIDLSSKHGGLFSFX | 60 |
| QY | 75 | FGSPPTVAASPTELFLFLQXHEATSPFTRPOTSAXBLTYDXXVAXXPKXPRYMXFVKL | 134 |
| Db | 61 | FGSPPTVAASPTELFLFLQTHETATSPNTRPQTSAIRRLTYDSSVAMVPFGPYMKFVKL | 120 |
| QY | 135 | IMNDLNAATTVXKLRLPLRTQOIRKQLRXMAQAEAKXPLDXTEBELKMXNSTXSMMLIGE | 194 |
| Db | 121 | IMNDLNAATTVXKLRLPLRTQOIRKLIRVMAQAAOKPLDTBELKMXNSTXSMMLIGE | 180 |
| QY | 195 | AEEIRDLARELKLTXGEYSLDTFHXPLKQLKVGEYKRIIDLINKEDPVNVRVTKKRXI | 254 |
| Db | 181 | AEEIRDLARELKLTXGEYSLDTFWPLKHLVGKYEKKIDILINKEDPVNVEVIKKREI | 240 |
| QY | 255 | VRRXKXNEXXKGEKSGVYLDTLFEPADETXEIKTKXXIXGLVVDXESAGXDSTAXXTE | 314 |
| Db | 241 | VRRKNGVIEGEYSGVFLDTLFEPADETXEIKTKHIXGLVVDFFSAGDSTAXVATE | 300 |
| QY | 315 | WALAEILNNPYVLXXAREEXYSVVGKDLVDEVDTONLPYIRAIKETFRMHPLPVYKR | 374 |
| Db | 301 | WALAEILNNPYVLKRAKEEYSVVGKORLVDEVDTONLPYIRAIKETFRMHPLPVYKR | 360 |
| QY | 375 | KCXEECKINGVXPDEGALXXFNVMQGXDKXRYMDPSPEXRPERFLEYAABEGAXLLDURG | 434 |
| Db | 361 | KCTEBCCEINGVVPDEGALLFNVMQVGRDPKXMDPSPSEFRPERFLEYAABEGARPLDURG | 420 |
| QY | 435 | XHFOLLPPGSGRXNCPGYXLTATSGKATLLAALIOCFDIQVIGPOGOLLKGDAXKSMER | 494 |
| Db | 421 | QHFOILLPPGSGRRNCPGVNLATSGMATLLAALIOCFDIQVIGPOGOLLKGDAXKSMER | 480 |
| QY | 495 | AGLTVPRAHSLVCVPLARIG 514 | |
| Db | 481 | AGLTVPRAHSLVCVPLARIG 500 | |

```

US-10-732-923-24071
RESULT 15
US-10-732-923-24071
Sequence 24071, Application US//10732923
Publication No. US20050108791A1
GENERAL INFORMATION:
APPLICANT: Edgetton, Michael D
TITLE OF INVENTION: TRANSGENIC PLANTS WITH
FILE REFERENCE: 38-15(52796) C
CURRENT APPLICATION NUMBER: US/10/732,923
CURRENT FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: 10/310,154
PRIOR FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 24149
SEQ ID NO 24071
LENGTH: 500
TYPE: PRT
ORGANISM: Lens culinaris
US-10-732-923-24071

```

| | | | | |
|---------------------------|-------|---------------------|-----------|-------------|
| Query Match | 91.0% | Score 2173; | DB 5; | Length 500; |
| Best Local Similarity | 86.4% | Pred. No. 4.8e-246; | | |
| Matches 432; Conservative | 0; | Mismatches 68; | Indels 0; | Gaps 0 |

QY 15 FYHIAPTPAKSKALRHLNPSPKPRPLPEFIGHXLKDKLHVAXIDLSKKHGPFPFSXX 74
Db 1 FHLHPPTPAKSKALRHLNPSPKPRPLPEFIGHPLHKKLHYALIDLSKKHGPFPFSLY 60
QY 75 FGSMEFTVAASTELEFKLFLQXXEATSFXTRFOTSAXKXILTYDXXVAXXFXGPKWAKVVRKL 134
Db 61 FGSMEFTVAASTELEFKLFLQTHAETSFNTRFOTSARILRLTYDSSVAMVFPFGPKWAKVVRKL 120
QY 135 IMNDLXNATTVXKLPRLPQQLRKILKRNAAQAAEAKKPLDXTHEILLKMNSTSTSMXKLE 194

```

Db      121  IMNDLNNATTVNKLRLPLRTOQIRKFLRVMAOSAEAKPLDVTBELKWTNSTISMMLGE 180
QY      195  ABEIDDIAREVVKIXGEYSLTDFIXPLKXKLVKGYEKRIDIDILNKPDVVERVKKRRXI 254
Db      181  ABEIDDIAREVVKIFGSISLTFIWLKYLKVGKTEKRIDIDILNKPDVVERVKKRRRI 240
QY      255  VRRRXNGEXXEGEXSGVXLDLLEFADETXEIKITKXXIXGLVVDXFSAGXSTAXXTE 314
Db      241  VRRRNGGEVVEGEAGVFLDITLLEFADETXEIKITKEQIKGLVVDXFSAGTDSATAVE 300
QY      315  WALAELINNPKVLLXXAREEXYSVVGKDXLVDEVDTQNLPIYRAIVKETFRMHPPLPVYKR 374
Db      301  WALAELINNPRVLQKAREEVSVVGKDLIVDEVDTQNLPIYRAIVKETFRMHPPLPVYKR 360
QY      375  KCXEECXINGXYXPEGALXXFNVWQVGVGDXXKYWDRPSEKXPERFLETXAEGAXXLDLRG 434
Db      361  KTECECEINGHYIPGALVYLFNVWQVGRDPKXTWDRSEFRFRFLETGAEGAGPLDLRG 420
QY      435  XHFQLLPFGSGRXMCPGVXLATSGXATLLASLIQCFDLQVLGPQGIILKGDAXVMEER 494
Db      421  QHFQLLPFGSGRMCPEGVNLATSGMATLLASLIQCFDLQVLGPQGIILKGDAXVMEER 480
QY      495  AGLTVPRAHSIVCVPLARIG 514
Db      481  AGLTVPRAHSIVCVPLARIG 500

```

Search completed: December 22, 2005, 00:15:11
 Job time : 116 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Comphen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: December 22, 2005, 00:15:20 ; Search time 283 Seconds
(without alignments)
955.390 Million cell updates/sec

Title: US-09-857-581b-66

Sequence: 1 MLELALGXVLAFLXHLRP.....ASHIVCPVARIQVSKLLS 521

Scoring table:

| | | |
|-------------|-------------|-------------|
| BLOSUM62 | Xgapop 10.0 | Xgapext 0.5 |
| Ygapop 10.0 | Ygapext 0.5 | |
| Delpop 6.0 | Delpext 7.0 | |
| Delop 6.0 | Delext 7.0 | |

Searched: 4168288 seqs, 259477437 residues

Total number of hits satisfying chosen parameters: 8336576

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+g2n.model -DEV=xlp
-Q=/cg21_1/USPRO.spool_p/US09857581/runat_15122005_083138_19467/app_query.fasta.1.711
-DB=published Applications NA New -QFMT=fastap -SUFFIX=trnbn -MINMATCH=0.1
-LOOPCT=0 -LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRN=human40.cdt -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09857581_@CGN_1_1_183_@runat_15122005_083138_19467
-NCPU=6 -ICPU=3 -NO MAP -LARGQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database:

Published Applications NA New:
1: /cg21_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
2: /cg21_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
3: /cg21_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
4: /cg21_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
5: /cg21_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
6: /cg21_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
7: /cg21_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
8: /cg21_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
9: /cg21_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
10: /cg21_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length DB | ID | Description |
|------------|-------|-------------|-----------|----|-------------------|
| 1 | 398 | 16.7 | 1690 | 6 | US-10-667-295-204 |
| 2 | 387.5 | 16.2 | 1799 | 6 | US-10-667-295-138 |
| 3 | 381.5 | 16.0 | 1794 | 6 | US-10-667-295-80 |
| 4 | 240.5 | 10.1 | 1509 | 6 | US-10-821-234-702 |
| 5 | 228.5 | 9.5 | 2623 | 6 | US-10-131-826A-63 |
| 6 | 225 | 9.4 | 3293 | 7 | US-11-112-908-17 |
| 7 | 191 | 8.0 | 1676 | 7 | US-11-102-240-53 |
| 8 | 190 | 8.0 | 1710 | 7 | US-11-000-463-641 |

| | | | | | | |
|----|-------|-----|--------|---|---------------------|--------------------|
| 9 | 190 | 8.0 | 1710 | 7 | US-11-000-463-642 | Sequence 642, App |
| 10 | 190 | 8.0 | 1710 | 7 | US-11-000-463-643 | Sequence 643, App |
| 11 | 187 | 7.8 | 1806 | 7 | US-11-000-463-169 | Sequence 169, App |
| 12 | 186.5 | 7.8 | 1473 | 6 | US-10-507-106-1 | Sequence 1, App1 |
| 13 | 183 | 7.7 | 1882 | 7 | US-11-000-463-170 | Sequence 170, App |
| 14 | 181 | 7.6 | 1685 | 6 | US-10-957-569-27 | Sequence 27, App1 |
| 15 | 180 | 7.5 | 2361 | 6 | US-10-995-561-81 | Sequence 81, App1 |
| 16 | 176 | 7.4 | 2361 | 6 | US-10-995-561-80 | Sequence 80, App1 |
| 17 | 176 | 7.4 | 2361 | 6 | US-10-995-561-82 | Sequence 82, App1 |
| 18 | 175.5 | 7.3 | 1547 | 7 | US-11-000-463-171 | Sequence 171, App |
| 19 | 161.5 | 6.8 | 1512 | 6 | US-10-821-234-675 | Sequence 675, App |
| 20 | 158 | 6.6 | 1934 | 6 | US-10-507-106-3 | Sequence 3, App1 |
| 21 | 157 | 6.6 | 2243 | 6 | US-10-131-826A-107 | Sequence 107, App |
| 22 | 150.5 | 6.3 | 1657 | 7 | US-11-186-284-225 | Sequence 225, App |
| 23 | 142.5 | 6.0 | 1566 | 6 | US-10-821-234-694 | Sequence 694, App |
| 24 | 124 | 5.2 | 95223 | 7 | US-11-117-187-188 | Sequence 188, App1 |
| 25 | 102.5 | 4.3 | 452 | 6 | US-10-667-295-38 | Sequence 38, App1 |
| 26 | 99 | 4.1 | 14172 | 7 | US-11-075-185-2 | Sequence 2, App1 |
| 27 | 97.5 | 4.1 | 1221 | 7 | US-11-075-185-53 | Sequence 53, App1 |
| 28 | 97.5 | 4.1 | 31973 | 6 | US-10-995-561-13229 | Sequence 13229, A |
| 29 | 89 | 3.7 | 1452 | 7 | US-11-112-908-284 | Sequence 284, App |
| 30 | 89 | 3.7 | 149111 | 7 | US-11-112-908-63 | Sequence 63, App1 |
| 31 | 89 | 3.7 | 157230 | 7 | US-11-112-908-64 | Sequence 64, App1 |
| 32 | 89 | 3.7 | 170508 | 7 | US-11-112-908-65 | Sequence 65, App1 |
| 33 | 89 | 3.7 | 173115 | 7 | US-11-112-908-65 | Sequence 65, App1 |
| 34 | 84.5 | 3.5 | 761 | 6 | US-10-497-135-18 | Sequence 18, App1 |
| 35 | 82.5 | 3.5 | 767 | 7 | US-10-497-135-17 | Sequence 17, App1 |
| 36 | 78 | 3.3 | 116856 | 7 | US-11-143-980-1 | Sequence 1, App1 |
| 37 | 77.5 | 3.2 | 530 | 7 | US-11-072-510-6 | Sequence 6, App1 |
| 38 | 77 | 3.2 | 1534 | 6 | US-10-750-185-38375 | Sequence 38375, A |
| 39 | 77 | 3.2 | 60486 | 6 | US-10-995-561-13310 | Sequence 13310, A |
| 40 | 76.5 | 3.2 | 1719 | 7 | US-10-750-185-61006 | Sequence 61006, A |
| 41 | 76 | 3.2 | 1917 | 7 | US-11-055-822-819 | Sequence 819, App |
| 42 | 76 | 3.2 | 2512 | 6 | US-10-750-185-49783 | Sequence 49783, A |
| 43 | 75 | 3.2 | 191684 | 7 | US-11-121-086-2 | Sequence 2, App1 |
| 44 | 75 | 3.1 | 18745 | 7 | US-11-121-086-83 | Sequence 83, App1 |
| 45 | 74.5 | 3.1 | 167891 | 7 | US-11-121-086-14 | Sequence 14, App1 |

ALIGNMENTS

RESULT 1
US-10-667-295-204
; Sequence 204, Application US/10667295
; Publication No. US20050257293A1
; GENERAL INFORMATION:
; APPLICANT: Masclia, Peter
; TITLE OR INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
; FILE REFERENCE: 11696-047001
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411, 823
; PRIOR FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 263
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 204
; LENGTH: 1690
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1690)
; OTHER INFORMATION: Ceres Seq. ID no. 12450440
US-10-667-295-204

Alignment Scores:
Pred. No.: 4.18e-43 Length: 1690
Score: 398.00 Matches: 136
Percent Similarity: 42.51% Conservative: 77
Best local Similarity: 27.15% Mismatches: 226
Query Match: 16.66% Indels: 63
DB: 6 Gaps: 18

[illegible]

```

QY      373  LysArgIysCys***GluGluCys***IleasnGly***Val***ProGluGluValAlaLeu 392
Db      1223  CCGCACATGAACCTTCGAGAGAGCGCAAGCTCGCGGCTACACCATCCCAAGAGGCTTCAG 128
QY      393  *****PheAsnValTTPrgIlnValGly***Asp***LysTyrTTPAsparPProSerGlu 412
Db      1293  GTGGTGTCAACGCGCTGTGTGGCTGGCCCAACAATCCGAGACTGTGGAGCAAGCCCGAGAG 134
QY      413  **ArgProGluArgPheLeuGluThr**AlaGluGlyGlnAla*****IleAspLeu 432
Db      1343  TTTCGGCCGAGCGGTTCTCTA-----GGGAGAGAGAAAGACCGTGGACGCGC 138
QY      433  Arg-----Gly**HisPheGlnIleuProPheGlySerGlyArg**MetCys 449
Db      1398  ACCGTGGCGGAGAGAGTGAAGTCTCCGCTTCCTCGCGCTTCGGCGTGGCGCGCGACCTGC 144
QY      450  ProGluVal**LeuAlaThrSerGly**AlaThrLeuAlaSerLeuIleGlnCys 469
Db      1448  CCGGGATCATCTTCGCGCTGCGCCATCCTCGGCGTCATGTGTGGCAAGCTCGTGGCGCAG 150
QY      470  PheAspLeuGlnValLeuGlyProGlnGlyGlnIleLeuLysGly**AspAlaLysVal 489
Db      1508  TTCAGATAGGT-ACCACCGCCCGCGGTGGAGAA----- 153
QY      490  SerMetGluGluArgAlaGlyLeuThrValProArgAlaHisSerLeuValCysValPro 509
Db      1540  GCTCAGCGTCACGAGAAAGAGACAGATTTCAGCTGCACAT-----TCCAACCA 159
QY      510  Leu 510
Db      1591  CTC 1593

RESULT 2
US-10-667-295-138
; Sequence 138, Application US/10667295
; Publication No. US20050257293A1
; GENERAL INFORMATION:
; APPLICANT: Mascoia, Peter
; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
; FILE REFERENCE: 11696-047001
; CURRENT APPLICATION NUMBER: US/10/667,295
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,823
; PRIOR FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 263
; SOFTWARE: FastSeq For Windows Version 4.0
; SEQ ID NO 138
; LENGTH: 1799
; TYPE: DNA
; ORGANISM: Glycine max
; NAME/KEY: misc_feature
; LOCATION: (1)...(1799)
; OTHER INFORMATION: Ceres Seq. ID no. 13531805
US-10-667-295-138

Alignment Scores:
Pred. No.:      1,236-41      Length:      1799
Score:          387.50      Matches:      135
Percent Similarity: 40.78%      Conservative: 73
Best Local Similarity: 26.47%      Mismatches:  227
Query Match:     16.22%      Indels:      75
Db:              6          Gaps:          15

US-09-857-581B-66 (1-521) x US-10-667-295-138 (1-1799)
QY      35  ProProSerPro**ProArgLeuProPheIleGlyHis**HisIleuLeuLysAspLys 54
Db      162  CCACCGGGGCCACCTCCCC---GTCCCAATCTTCGGCAACTGGGCTCCAGTCCGCGCAGAC 218
QY      55  LeuLeuHisTyrAla***IleAspLeuSerLysLysGlyProLeuPheSer***** 74

```

```

Db      219 CTCACACCGCAACCTTCCATTTGGCCAAAATTCGGTGACATCTTCTCCGCG 278
Qy      75 PheGlySerMetProThrValAlaSerThrProGluLeuPheLeuPheLeu 94
Db      279 ATGGGCGACGCAACCTCGTGGTGTCTTCCCTGGAGCTCCGCAAGAGGTTCTCCAC 338
Qy      95 ****GluAlaThrSerPhe***ThrArgPheGlnThrSerAla***Arg***LeuThr 114
Db      339 ---ACCGAGGCGCTGAGATTCCGCTCCGCG-----ACCGCAACGTCGTC 380
Qy      115 TyrAsp-----*****ValAla*****Pro***GlyProTyrTrp 128
Db      381 TTCGACATCTTCAACCGAAAGGCGCAAGATGTCCTTCAACCTCTACCGCGGACATCG 440
Qy      129 ***PheValArgLysLeuIleMetAsnAspLeu***AsnAlaThrThrValAsn***Leu 148
Db      441 CGCAAAATGCGCGGCATCATG-----ACCGTCCCTCTTCTC 476
Qy      149 ArgProLeuArgThrGlnGlnIleArg----- 157
Db      477 ACCAACAGGTGTGGCAACATACCGCATGATGGGAATCGAGAGCTGCGCGCTGTC 536
Qy      158 Lys***LeuArg***MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGlu 177
Db      537 GAGGACGTCAAGAAAACCCCGACGCGCTCCGCGCACCCGTCATCCGCGCGCTT 596
Qy      178 GluLeuLeuLysTrp***AsnSerThr***SerMetMet***LeuGlyGluAlaGlu 197
Db      597 CAGCTCATGATGTACCAACATGTACCGCATATATTTGCAACGAGGTTTGAGAGCGGAG 656
Qy      198 IleArgAspIleAlaArgGluValLeuLysIle***Gly----- 210
Db      657 GAGATCCCATCTTCCAGAGCTTAAAGCCTTGAACGAGAGAGAGTCCGTTGGCGCAG 716
Qy      211 -----GluTyrSerLeuThrAspPheIle***ProLeuLys----- 223
Db      717 AGCTTGAGTATTACTATGTGATTTATTTATCCATCTTGAGACCTTCTTGAAAGGTTAC 776
Qy      224 LeuLysValGlyLysTyrGluLysArgIleAspAspIleLeuAsnLysPheAspProVal 243
Db      777 TTGAAGATTTTGCAGAGGTCAGAGTCAGAGGTTGAAGCTTTTCAAGAGATTACTTCGTT 836
Qy      244 ValGluArgValIleLysLysArgArg***IleValArgArgArg***AsnGlyGlu*** 263
Db      837 GACCAAGAG-----AAGAGCTTGAAGACCAAGACCAACCAACAAATATGA--- 887
Qy      264 **GluGlyGlu***SerGlyVal***LeuAspThrLeuLeuGluPheAlaGluAspGlu 283
Db      888 -----CTTAATGCGCTATTGACCAATTTTGATGCC 920
Qy      284 Thr**GluIleLysIleThrLys*****Ile***GlyLeuValValAsp***PheSer 303
Db      921 CAGAGAAAAGCGGATCAAGAACACAAACGCTCTTCACTGTTGAAGAAATCAACGCTT 980
Qy      304 AlaGly***AspSerThrAla*****ThrGluTrpAlaLeuAlaGluLeuIleAsnAsn 323
Db      981 GCTGCAATTGAAACAATCTATGTGTCATGTAGTGGGCAATTCCTGAGCTTGTGAACAC 1040
Qy      324 Pro**ValLeu*****AlaArgGluGlu***TyrSerValValGlyLysAsp***Leu 343
Db      1041 CCAGAGATCCAGCAAAAGTTAAGGATGAGATTGACAGAGTTCTTGAGAGCGGACCCAA 1100
Qy      344 ValAspGluValAspThrGlnAsnLeuProTyrIleAsnAlaIleValLysGluThrPhe 363
Db      1101 GTGACTGCGCAGACATCCAAAAGCTCCATACCTCCCAAGCAGTGGTCAAGAAATCTTT 1160
Qy      364 ArgMetHisProProLeuPro---ValValLysArgLysCys***GluGlyCys***Ile 382
Db      1161 CGTCTTAATAGCAATCCCTCTCTCTGTACACACATGAACCTCCAGACGCAAAAGCTT 1220
Qy      383 AsnGly***Val***ProGluGlyValLeu*****PheAsnValTrpGlnValGly*** 402
Db      1221 GGGGGCTATGATATCCAGCTGAGAGCAAGATCTTGATGATGATGATGATGATGATGAT 1280

```

```

Qy      403 Asp***LysTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGlnThr*** 422
Db      1281 AACCTGCACACTGGAGAAAGCCAGAGAGTTCGCGCTCGAAGAGTTCCTTTCAG----- 1334
Qy      423 AlaGluGlyGluAla*****LeuAspLeuArgGly***HisPheGlnLeuLeuProPhe 442
Db      1335 -----GAGAGTCCGCTGTGTGAAGCCAAATGGCAATGACTTTTAGTACCTTCCCTTT 1385
Qy      443 GlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***AlaThrLeu 462
Db      1386 GGTGTGGCAGAAAGAGCTCCCTGGAATCATCTTGAATGCAATTCGCAATTCGACATCAT 1445
Qy      463 LeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnLysGlnIleLeu 482
Db      1446 TTGGAGCGTTGGTCCAAAATCTTGAGCTC-----TTCCCTCCCGCTGGCGCAG----- 1493
Qy      483 LysGly***AspAlaLysValSerMetGluGluArgAlaGly-----LeuThrVal 499
Db      1494 -----TCACAGATGACACTAGTGAAGAAAGAGGCAATTTAGCTTGCACATA 1541
Qy      500 ProArgAlaHisSerLeuValCysValPro 509
Db      1542 CTCACGATTCACCACTTGTGGCAAGCCA 1571

RESULT 3
US-10-667-295-80
; Sequence 80, Application US//10667295
; Publication No. US20050257293A1
; GENERAL INFORMATION:
; APPLICANT: Mascia, Peter
; TITLE OF INVENTION: BIOLOGICAL CONTAINMENT SYSTEM
; FILE REFERENCE: 11696-047001
; CURRENT APPLICATION NUMBER: US/10/667,295
; PRIOR FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 80
; LENGTH: 1794
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1794)
; OTHER INFORMATION: Ceres Seq. ID no. 12558789
US-10-667-295-80

Alignment Scores:
Pred. No.:      8e-41      Length:      1794
Score:          381.50     Matches:      137
Percent Similarity: 41.79%   Conservative: 82
Best Local Similarity: 26.15%  Mismatches: 236
Query Match:    15.97%     Indels:      69
DB:              6        Gaps:      19

US-09-857-581b-66 (1-521) x US-10-667-295-80 (1-1794)
Qy      1 MetLeuLeuGluLeuAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeuArgPro 20
Db      97 CTCCTTGTCTGGAGAGTCTTTA-----ATCCCGCTCTTCGTCGGCGGTATCTC 144
Qy      21 ThrPro**Ala***SerLysAlaLeuArgHisLeuProAsnProProSerPro**Pro 40
Db      145 GCCACGGTGAATTTGAAGCTCCGCGGCAAGAAATTTGAAGTACCTCCAGGTCCTATACCA 204
Qy      41 ArgLeuProPheIleGlyHis***HisLeuLeuLysAspLysLeuLeuHisTyrAla*** 60
Db      205 ---ATTCGATCTTCGAAACTGGCTTCAAGTCGAGATGATATCAACACCGTAATCTC 261
Qy      61 IleAspLeuSerLysLysHisGlyProLeuPheSer*****PheGlySerMetProThr 80

```

```

Db      262 GTCGATTACGCTAAGAAATTCGGCGAATCTCTCTCCGTATGGGTACGAAACCTA 321
QY      81 ValValAlaSerThrProGluLeuPheLysLeuPheLeuGln*****GluAlaThrSer 100
Db      322 GTCGTGCTCTCCCTACCGCGATCTTAACAAGAAAGTGCTC---CTCACTCAAGCGTTGAG 378
QY      101 Phe***ThrArgPheGlnThrSerAla***Arg***LeuThrTrpAsp----- 116
Db      379 TTTCGATCCAGA-----ACGAGAAAGCGTGTTCGACATTTTCACCCGGG 423
QY      117 *****ValAla*****Pro**GlyProTrpTrp**PheValArgLysLeu 134
Db      424 AAGGTCACAGATATGGTTCACCTGTTTACGGCAGCATTTGAGAGAAATGAGAAATC 483
QY      135 IleMetAsnAspLeu***AsnAlaThrThrValAsn***LeuArgProLeuArgThrGln 154
Db      484 ATG-----ACGGTTCCTTTCTTCCACCAACAAAGTTGTTCAA 519
QY      155 GlnIleArgLys***LeuArg-----MetAlaGln**AlaGluAla**Lys----- 171
Db      520 CAGAAATCGTACAGCTTGGAGATTGAAAGCAGCTTAGTGTGTAAGATGTTAAGAAAT 579
QY      172 ProLeuAsp***ThrGlu-----GluLeuLeuLysTrp** 183
Db      580 CCAGATTCCTGCTACGAAAGAAATCGTGTGAGAAACGTTTGCATTTGATGATGATTAAC 639
QY      184 AsnSerThr***SerMetMet***LeuGlyGluAlaGluGluIleArgAspIleAlaArg 203
Db      640 AATATGTTCCGTATCATGTTGATAGAAAGATTTGAGAGTGAAGATGATCTCTTTTCCT 699
QY      204 GluValLeuLysIle**Gly-----GluValLeuLysLeu 214
Db      700 AGGCTTAAGCTTGAATGAGTGTGAGAAAGTCGATTAAGCTCAGACCTTGGATTAACAT 759
QY      215 ThrAspPheIle**ProLeuLys**LeuLysValGlyLysTrpGluLysArgGlyLeu 234
Db      760 GGAGATTTTCATCTCTTACCTTAGACCATTCCTCAGAGGC---TATTGAAGATTTCGAA 816
QY      235 AspIleLeuAsnLysPheAspProValValGluArg---ValIleLysLysArgArg** 253
Db      817 GATGTGAAGATCGAAGAAATCGCTCTTTTCAGAAAGATCTTGTGTGTGAGAGAAACAA 876
QY      254 IleValArgArgArg**AenGlyGlu*****GluGlyGlu**SerGlyVal**Leu 273
Db      877 ATTGCGAGTTCTTAAGCTTACAGGT-----AGTGAAGATGGAATGTCAT 924
QY      274 AspThrLeuLeuGluPheAlaGluAspGluThr**GluIleLysIleThrLys***** 293
Db      925 GATCACAATCTCTGA---GCTGAGCAGAGAGGA-----GAAATCAACGAGACAAAT 972
QY      294 Ile***GlyLeuValValAsp***PheSerAlaGly**AspSerThrAla*****Thr 313
Db      973 GTTCTTTACATCGTCGAGAAATCATCAATGTGCGCCGATTTAGACAAACATTTGTGTCATC 1032
QY      314 GluThrAlaLeuAlaGluLeuIleAsnAsnPro***ValLeu*****AlaArgGluGlu 333
Db      1033 GAAGTGGGAATTTGACAGCTAGTAGAACATCTCAAAATCCAGAGTAAGCTTAAGAGACGA 1092
QY      334 ***TyrSerValValGlyLysAsp**LeuValAspGluValAspThrGlnAsnLeuPro 353
Db      1093 CTCGACACAGCTTCTTGACCGGGGTGTCAGATCACCGACCTGATCTTCAAAACCTTCCA 1152
QY      354 TyrIleArgAlaIleValLysGluThrPheArgMetHisProProLeuPro---ValVal 372
Db      1153 TACCTTAAGCTGTGTTAAGAGACATCTTCGTGTGAATGCGGCAATTCCTCTCTGTG 1212
QY      373 LysArgLysCys**GluGluCys**IleAsnGly**Val***ProGluGlyAlaLeu 392
Db      1213 CTCACACATGAACCTCCATGATGCGAAGCTGCTGGCTACGATATCCACGACAAAGCAAA 1272
QY      393 *****PheAsnValTrpGlnValGly**Asp***LysTrpTrpAspArgProSerGlu 412
Db      1273 ATCTTGTATATGCTGTGTGTGCTTACGAAACAAACCCCAACAGCTGAGAAAGCTGAGAG 1332

```

```

QY      413 ***ArgProGluArgPheLeuGluThr***AlaGluGlyGluAla*****LeuAspLeu 432
Db      1333 TTTCAGCCAGAGAGGTTCTTTGAA-----GAAAGATCGACGTTGAAGCT 1377
QY      433 ArgGly**HisPheGlnLeuLeuProPheGlySerGlyArg***MetCysProGlyVal 452
Db      1378 AACGGTAAATGACTTTCAGGTAATGTGCATTTGGGTGTGAGACGTGCAAGCTGTCGGGAT 1437
QY      453 ***LeuAlaThrSerGly**AlaThrLeuLeuAlaSerLeuIleGlnCysPheAspLeu 472
Db      1438 AATATGGCAATTCCTTAATTTTGGGAGATCAACCATTTGGATGATGATCCAGAACTTCAG 1497
QY      473 GlnValLeuGlyProGlnIleGlnIleLeuLysGly**AspAlaLysValSerMetGlu 492
Db      1498 -----CTTCCTCTCTCAGAGCAG-----TCTAAATGATGATCTACT 1533
QY      493 GluArgAlaGly 496
Db      1534 GAGAAAGGTGGA 1545

RESULT 4
US-10-821-234-702
/ Sequence 702, Application US/10821234
/ Publication No. US20050255114A1
/ GENERAL INFORMATION:
/ APPLICANT: Labat, Ivan
/ APPLICANT: Stachne-Crain, Birgit
/ APPLICANT: Andarmani, Susan
/ APPLICANT: Tang, Y. Tom
/ TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
/ FILE REFERENCE: 821A
/ CURRENT APPLICATION NUMBER: US/10/821,234
/ CURRENT FILING DATE: 2004-04-07
/ PRIOR APPLICATION NUMBER: US 60/462,047
/ PRIOR FILING DATE: 2003-04-07
/ NUMBER OF SEQ ID NOS: 1704
/ SOFTWARE: pc_seq_genes Version 1.0
/ SEQ ID NO 702
/ LENGTH: 1509
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-821-234-702

Alignment Scores:
Pred. No.: 9,21e-22 Length: 1509
Score: 240.50 Matches: 120
Percent Similarity: 37.80% Conservative: 83
Best Local Similarity: 22.35% Mismatches: 261
Query Match: 10.07% Indels: 73
DB: 6 Gaps: 20

US-09-857-581b-66 (1-521) x US-10-821-234-702 (1-1509)
QY      6 AlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeuArgProThrPro----- 22
Db      10 GCGATGGCTCTGTGGCGGGGTGCGCTGTGGAGAGGTGCATCTTCTGCACTCTACTG 69
QY      23 -----***Ala***SerLysAlaLeuArgHisLeuProAsn----- 34
Db      70 GGCACGTGCGCTTCTGTGCTGCTGCTGACTTCTTCAAAAGCGGCGCCCAAGAACTAC 129
QY      35 ProProSerPro**ProArgLeuProPheIleGlyHis***HisLeuLysAspLys 54
Db      130 CGCGCGGGGCGCTCG---CGCTGCGCTTCTTGGCAACTTCTTCTTGTGACCTTCGAG 186
QY      55 LeuLeuHisGlyAla***IleAspLeuSerLysLysHisGlyProLeuPheSer***** 74
Db      187 CAGTCGCACTCGAGGTTGACGCTGTTGTGAAGAAATATAGGGAACCTTTTACCTTGAGAG 246
QY      75 PheGlySerMetProThrValValAlaSerThrProGluLeuPheLysLeuPheLeuGln 94
Db      247 CTGGTGACATATATCTCAGTCTTATTAAGCTTCCCTTAATCAAAAGAACCTTATTC 306

```


| | | | |
|------------------------|--------|---------------|-----|
| Score: | 226.50 | Matches: | 118 |
| Percent Similarity: | 38.97% | Conservative: | 78 |
| Best Local Similarity: | 23.46% | Mismatches: | 230 |
| Query Match: | 9.48% | Indels: | 77 |
| DB: | 6 | Gaps: | 21 |

US-09-857-581B-66 (1-521) x US-10-131-826A-63 (1-2623)

[illegible]

| | | | | | | | |
|--|----------|---------------|--|------|----|--|-----|
| D6 | | : | : :: : | :: | :: | 908 AAGAACATGCTGATGAACGTATTATTTCCTGGTGCAGATGACCGTTACAGCC | 967 |
| OY | | | **Thrglurtpalaleualaglu.leu]easna\$Pro**Valleu*****Alarg | 331 | | | |
| D6 | | | 968 ACGGTGCGCCTAACCCTTCCTGCTCTCATGAAATACCTCATGTCMAAAGTGGTAGCT | 1027 | | | |
| OY | | | 332 GlUglu***TySerValVla]gLyLysasp***LeuVal]spGlUval]AsPThrGlnasn | 351 | | | |
| D6 | | | 1028 GAGAAGCTGTAATCCGGAGCTGGGGGCTGGCCAGCACCAAGCCTAGGGGACCGTAGCCGC | 1087 | | | |
| OY | | | 352 LeuProTrylrlea]ga]ai]evall]yegLuThrPhearpmethisProProLeuProVal | 371 | | | |
| D6 | | | 1088 CTCCCTTACACCGACGCGGTTCATGAGGCCAGCGCGCTGGCGCGCTGCCTCATG | 1147 | | | |
| OY | | | 372 --'Vallysar]gLyCyS***GlUglucyS***I]easn]y***Val**Proglugly | 390 | | | |
| D6 | | | 1148 GAATPATCCCCGACCCCTCATGCGGACACACCCGCTTCGAGAGGTACACCTGCCACAGGC | 1207 | | | |
| OY | | | 391 AlAleu*****PhebasnValTPRplnValgLy]**asp***LySrTYTRPaSPArgPro | 410 | | | |
| D6 | | | 1208 ACGAGGCTCTCCCCTCTGGCTGCATCGCATACCCCAACATCTTCAGACACCCA | 1267 | | | |
| OY | | | 411 Ser]gu***ArGPpro]uar]gPhe]eu]gnJurthr**AlaglUgl]yu]a]a****Leu | 430 | | | |
| D6 | | | 1268 GAAGGTTCAACCCAGACCGTTCCTGGAT-----GCAGTGAACGGTTACG---- | 1315 | | | |
| OY | | | 431 AspleuAr]gLy**HisphelnleuLeuProPhe]ySer]giYar]**MetCysePro | 450 | | | |
| D6 | | | 1316 -----AAGCATGAGCGCTCTGCTCTTCCTTCTAGGGAAGCGTCTGCCTT | 1363 | | | |
| OY | | | 451 GlYva]**Teua]atmrSer]gy**AlatrleuLeualaSerleu]legncySphe | 470 | | | |
| D6 | | | 1364 GGAAGAGGCGCTCGCAAAGCGAGACTCTTCCTCTTCTTCAACCAACATCTTCAAGCCCTTC | 1423 | | | |
| OY | | | 471 Asp]eu]gn | 473 | | | |
| D6 | | | 1424 TCCTCGAG | 1432 | | | |
| RESULT 6 | | | | | | | |
| US-11-112-908-17 | | | | | | | |
| Sequence 17, Application US/11112908 | | | | | | | |
| Publication No. US20050260659A1 | | | | | | | |
| GENERAL INFORMATION: | | | | | | | |
| APPLICANT: Harris, Cole | | | | | | | |
| TITLE OF INVENTION: Breast Cancer Biomarkers | | | | | | | |
| FILE REFERENCE: 04-164-US | | | | | | | |
| CURRENT APPLICATION NUMBER: US/11/112, 908 | | | | | | | |
| CURRENT FILING DATE: 2005-04-22 | | | | | | | |
| PRIOR APPLICATION NUMBER: US 60/564, 758 | | | | | | | |
| PRIOR FILING DATE: 2004-04-23 | | | | | | | |
| PRIOR APPLICATION NUMBER: US 60/575, 978 | | | | | | | |
| PRIOR FILING DATE: 2004-06-01 | | | | | | | |
| PRIOR APPLICATION NUMBER: US 60/631, 702 | | | | | | | |
| PRIOR FILING DATE: 2004-11-30 | | | | | | | |
| PRIOR APPLICATION NUMBER: US 60/633, 826 | | | | | | | |
| PRIOR FILING DATE: 2004-12-07 | | | | | | | |
| NUMBER OF SEQ ID NOS: 511 | | | | | | | |
| SOFTWARE: PatentIn version 3.3 | | | | | | | |
| SEQ ID NO 17 | | | | | | | |
| LENGTH: 3295 | | | | | | | |
| TYPE: DNA | | | | | | | |
| ORGANISM: Homo sapiens | | | | | | | |
| US-11-112-908-17 | | | | | | | |
| Alignment Scores: | | | | | | | |
| Pred. No.: | 3,74e-19 | Length: | 3295 | | | | |
| Score: | 225.00 | Matches: | 108 | | | | |
| Percent Similarity: | 36.11% | Conservative: | 83 | | | | |
| Best Local Similarity: | 20.42% | Mismatches: | 218 | | | | |
| Query Match: | 9.42% | Indels: | 120 | | | | |
| DB: | 7 | Gaps: | 16 | | | | |

```

US-09-857-581b-66 (1-521) x US-11-112-908-17 (1-3295)
QY 32 LeuProAsnProProSerPro***ProArgLeuProPheIleGlyHis***HisLeuLeu 51
DB 578 CTGCGCGGCGCCACGAC-----TGGCACCTGCTGGGC-----ACCTGCTG 619
QY 52 LysAsp-----LysLeuLeuHisTyrAla***IleAspLeuSerLys 65
DB 620 CAGATTCTCGAAGGGGCTCCAGAAACAGACAGACCCGTGGAGTACCAAG 679
QY 66 LysHisGlyProLeuPheSer****PheGlySerLeuProThrValAlaIleSerThr 85
DB 680 AAGTATGGCAAGATTTCGCGATGAAAGTTGGTTCCTTGTGCTGGGACCTGGGCTCG 739
QY 86 ProGluLeuPheLysLeuPheLeuGln****GluAlaThrSerPhe***ThrArgPhe 105
DB 740 CCATGCTGCTGGAAGGCTGTACCGACGAGAGCGCG----- 778
QY 106 GlnThrSerAla***Arg***LeuThrTyrAsp****ValAla****Pro***Gly 125
DB 779 -----TACCCGAGCGGCTGGAGATCAACCGTGAAG 811
QY 126 ProTyrTrp***PheValArgLys-----LeuIleMetAsnAspLeu***AsnAla 142
DB 812 GCCTATCGCGACTACCGCAAGAGGCTACGGGCTGCTGATC----- 853
QY 143 ThrThrValAsn***LeuArgProLeuArgThrGlnIleLeuArgLys***LeuArg*** 162
DB 854 -----CTGGAAAGGGGAAAGACTGCGAGCGGGCTCGAGTGCCTTTCAA-- 895
QY 163 MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGluLeuLeuLysTrp 182
DB 896 -----AAGAACTAATGAAACAGGGGAAAGTATGAAGCTG 931
QY 183 ***AsnSerThr***SerMetMet***-----LeuGlyGluAlaGluGlnIleArgAsp 200
DB 932 GACAAACAATTCATAGAGTCTTGCGCGATTTATGGGACGAATAGATGAGCTGTGAT 991
QY 201 IleAlaArgGluValLeuLysIle***GlyGluTyrSerLeuThrAspPheIle***Pro 220
DB 992 GAAAGAGCGCACGTCGAGAACTTGTACAGCACTGAAACAATGTCGTGTT----- 1042
QY 221 LeuLys***LeuLysValGlyLysTyrGluLysArgIle----- 233
DB 1043 ---GAAAGTATCTGCTGCTGCTGTGTATGAGAGAGATTGGGCTTCCAGAAATGCA 1099
QY 234 ---AspAspIleLeuAsnLysPheAspProValValGluArgValIleLysLysArgArg 252
DB 1100 GGGGATGAAGCTGGAAGTTCATCATGAGCCATCAAAACAATGATGAGACGTTGGAGG 1159
QY 253 ***IleVal]-----ArgArgArg***AsnGlyGlu****GluGlyGlu 267
DB 1160 ATGATGTCACCTCAGTCAGAGCTCAGCAAGAGCTCAACAAGAGTCTGCGAGGACAC 1219
QY 268 ***SerGlyVal***LeuAspThrLeuLeu----- 277
DB 1220 ACT-----CTGGCCTGGGACACCATTTTCAATCATGCTCAAGCTGTATGACAAACCG 1273
QY 278 -----GluPheAlaGluAspGluThr**GluIle 287
DB 1274 TTAGAGAGATATTCAGACGACCTAGTCAGATTTCTTTGTGACATTATCACAGAT 1333
QY 288 LysIleThrLys****Ile***GlyLeuValValAsp***PheSerAlaGly***Asp 307
DB 1334 CGGCTTTCAGAAAGAAATGTATGCTGCTGTCAAGAGCTTCAGAGCTGGCGGTGAA 1393
QY 308 SerThrAla*****ThrGluTrpAlaLeuAlaGluLeuIleAsnAspPro***ValLeu 327
DB 1394 ACGACAGCAAAACGCTAATGTGATTTCTTCAATTTATCCCGTAATCCCAAGCTGAA 1453
QY 328 *****AlaArgGluGlu***TyrSerValValGlyLysAsp***LeuValAspGluVal 347

```

```

DB 1454 CAAAGCTTCTTAGGAATTCGAAGTATTAACCTGAGAAATCAGTGCCAGCGGCAAA 1513
QY 348 AspThrGlnAsnLeuProTyrIleArgAlaIleValLysGluThrPheArgMetHisPro 367
DB 1514 GATTGAGGAATATATCGGATATTAAAGCTCTCGAAGAAATCTATAGAGCTTACGCCG 1573
QY 368 ProLeuProValValLysArgLysCys***GluGluCys***IleAsnGly***Val*** 387
DB 1574 AGTGATCACTTTTACCACTCGAGCTTTCAGAAAGGCAACAGTTCTGGTGAATATGCTTAA 1633
QY 388 ProGluGluValAlaLeu*****PheAsnValTrpGlnValGly***Asp***LysTyrTrp 407
DB 1634 CCAAGAGAACAGTGTCTATGCTAAATACCAAGCTTGGAGTCCAGTGAAGCAATTTT 1693
QY 408 AspArgProSerGlu***ArgProGluArgPheLeuGluThr***AlaGluGlyGluAla 427
DB 1694 GAAGATTCAAGTACAGTTTGAAGCTGTAACCTTGAGCTTCAG-----GAGAAAGAA-- 1741
QY 428 *****LeuAspLeuArgGly***HisPheGlnLeuLeuProPheGlySerGlyArg*** 447
DB 1742 -----AAATTAATCCTTTTGGCATCTTCATTGCGCTGGAAAAAGA 1786
QY 448 MetCysProGlyVal***LeuAlaThrSerGly***AlaThrLeuLeuAlaSerLeuIle 467
DB 1787 ATGTGATTTGTGCGCGATTAAGCAGAGCTTCAACTGCATTGGCTCTTTGTGATTTGTC 1846
QY 468 GlnCysPheAspLeuGlnValLeuGlyProGlnGlyGlnIleLeuLysGly***AspAla 487
DB 1847 CGGAATATGACATCCACGCGCACAGCAATGAG----- 1879
QY 488 LysValSerMetGluGluArgAlaGlyLeuThrValProArgAlaHisSerLeuValCys 507
DB 1880 -----CCTGTGAGATGCTACACTCACTGAGCACCCTTG 1909
QY 508 ValProLeuAlaArgIleGlyValAla 516
DB 1910 GTGCCAGCGCGGAACCTCCCATGCGC 1936

```

RESULT 7

US-11-102-240-53

Sequence 53, Application US/11102240

Publication No. US20050260647A1

GENERAL INFORMATION:

APPLICANT: Goddard, Audrey J.

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, Christopher J.

APPLICANT: Gurney, Austin L.

APPLICANT: Wood, William I.

TITLE OF INVENTION: ANTIBODIES TO POLYPEPTIDES ENCODED BY A NUCLEIC ACID UNDEREXPRES

FILE REFERENCE: P3230R1C106C

CURRENT APPLICATION NUMBER: US/11/102,240

CURRENT FILING DATE: 2005-04-08

PRIOR APPLICATION NUMBER: 10/063662

PRIOR FILING DATE: 2002-05-07

PRIOR APPLICATION NUMBER: 10/006867

PRIOR FILING DATE: 2001-12-06

PRIOR APPLICATION NUMBER: PCT/US00/23328

PRIOR FILING DATE: 2000-08-24

PRIOR APPLICATION NUMBER: 60/170262

PRIOR FILING DATE: 199-12-09

NUMBER OF SEQ ID NOS: 170

SEQ ID NO 53

LENGTH: 1676

TYPE: DNA

ORGANISM: Homo Sapien

US-11-102-240-53

Alignment Scores:

| | | | |
|------------------------|----------|---------------|------|
| Pred. No.: | 5,78e-15 | Length: | 1676 |
| Score: | 191.00 | Matches: | 115 |
| Percent Similarity: | 34.03% | Conservative: | 63 |
| Best Local Similarity: | 21.99% | Mismatches: | 239 |

```

Query Match:      7.99%      Indels:      106
DB:               7          Gaps:         21
US-09-857-581b-66 (1-521) x US-11-102-240-53 (1-1676)

QY      1 MetLeuLeuGluLeuAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeuArgPro 20
      99 CTACTCTGCTGCTGGTGTGGGCTCTGCTGCTACTCGCC-----CCCATCTGGCT 149
QY      21 ThrPro***Ala***SerIysAlaLeuArgHisLeuProAsnProProSerPro***Pro 40
      150 TGGACCTATGCTTCTATTAACAACCTGCCGCGCTCAAGTGTTCACAGAGCCCAAAA 209
QY      41 ArgLeuProPheIleGlyHis***HisLeu-----LeuLysAsp 53
      210 CGGAACGCTGTTTGGGGTCACTGGGCTGATCACTCTACAGAGAGGGCTTGAAGAC 269
QY      54 LysLeuLeuHisTyrAla***IleAspLeuSerLysHisGlyProLeuPheSer*** 73
      270 -----TCGACCCAGATGTGGGCACCTATTCACAGGCGCTTACCGTA 311
QY      74 ***PheGlySer---MetProThrValAlaIleSerThrProGluLeuPheLysPhe 92
      312 TGGCTGGGTCCCATCATCCCTTCATGTTTATGCAACCTGACACCATCCGCTATC 371
QY      93 LeuGln***GluAla-----ThreSerPhe***ThrArgPheGlnThrSer 108
      372 ACCAATGCCCTCAGCTGCATTCGACCCAGAGATTACTCTTCATCAGGTTT----- 422
QY      109 Ala***Arg***LeuThrTyrAsp*****ValAla*****Pro----- 123
      423 -----CTGAAGCCCTGGCTGGAGAGG 446
QY      124 -----***GlyProTyrTrp***PheValArgLysLeuIleMetAsnAspLeu 139
      447 ATACTGCTGAGTGGCGGTGACAAGTGAAGCGCCGACGCTGGAG-----CTG 494
QY      140 ***AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys*** 159
      495 AGCGCCGCTTCCATTCACATCCATCAAGTCCATATTAAG---ATCTTCACACAGAGT 551
QY      160 LeuArg***MetAlaGln-----***AlaGluAla***LysProLeuAsp 174
      552 GCAAACTCATGCTTGACAAGTGGACAGCACCTGCTCAAGAGGAGGACAGCTGCTGAC 611
QY      175 ***ThrGluLeuLeuLysTyr***AsnSerThr***SerMetMet***LeuGlyGlu 194
      612 ATGTTTGAGCAGATC-----AGCTCATGACCTTGACAGT 647
QY      195 AlaGluGlu---IleArgAspIleAlaArgGluValLeuLysIle***GlyLysTyrSer 213
      648 CTACAGAAATGCATCTTCAGCTTGACAGCATTGTGAGAGAGGCCAGTAATATTT 707
QY      214 LeuThrAspPheIle***ProLeuLys***LeuLysValGlyLysTyrGluLysArgIle 233
      708 GCCACC-----ATCTTGAGCTCAGAGCCCTT-----GTAGAGAAAGAAGC 749
QY      234 AspAspIleLeuLysHisPheAsp----- 241
      750 CAGCATATCTCTCCAGACATGACTTCTGTATTACTCTCCCATGACGGGCGGCTTC 809
QY      242 -----ProValGluArgValIleLysLysArgArg*** 253
      810 CACAGGGCTGCGCCCTGCTGATGACTTCACAGACCGCTGATCCGGAGCGGCGTCC 869
QY      254 IleValArgArgArg***AsnGlyGlu***GluGlyGlu***SerGlyVal***Leu 273
      870 ACCCTCCCACTCAGGGATTTGATGATTTTCAAGAACAAGCAAGTCCAAAGACTTG 929
QY      274 Asp-----ThrIleLeuGluPheAlaGluAspGluThr***GluIleLysIleThrLys 291
      930 GAATTCATGATGTGCTTGTGCTGAGCAAGATGAAGTGGAG---GCATTGTCAAT 986

```

```

QY      292 *****Ile***GlyLeuValValAsp***PheSerAlaGly***AspSerThrAla*** 311
      987 GAGATATTAAGACAGAGGCTGACACCTTCATGTTTGGAGGCGCATACACAGGCGCAGT 1046
QY      312 ***ThrGluTrpAlaLeuAlaGluLeuIleAsnAspPro***ValLeu*****AlaArg 331
      1047 GGCCTCTCCTGGGTCTGTACAACTTGGCGAGGACCCAGAAATACAGAGGCGCTCCGA 1106
QY      332 GluGlu***TyrSerValValGlyLysAsp***LeuValAspGluVal-----Asp 348
      1107 CAGAGGTGCAAGAGCTTCTG---AAGGACCGGATCTTAAGAGATTAATGAGACAGC 1163
QY      349 ThrGlnAsnLeuProTyrIleArgAlaIleValLysGluThrPheArgPheHisProPro 368
      1164 CTGGCCAGCTGCTCTTCTGACCATGTGCGTGAAGAGAGCTGAGTTACATCCCCCA 1223
QY      369 LeuProValValLysArgLysCys***GluGluCys***Ile---AsnGly***Val*** 387
      1224 GCTCCCTTCAATCCCGATGCTGACACCCAGACATTTGTTCTCCAGATGCGCGATCATC 1283
QY      388 ProGluGlyAlaLeu*****PheAsnValTrpGlnValGlyY***Asp***LysTyrTrp 407
      1284 CCCAAGGCAATTAATCTGCTCATGATTAATTAAGGCTCATACACCAACTGTGTG 1343
QY      408 AspArgProSerGlu***ArgProGluArgPheLeuGlnThr***AlaGluGlyGluAla 427
      1344 CCGATCTTGAGGCTTACGACCCCTTCCGCTTGAACCAAGAAACAGCAAGGAGGTCA 1403
QY      428 *****LeuAspLeuArgLys***HisPheGlnLeuLeuProPheAspLysSerGlyArg*** 447
      1404 -----CCTGCGCTTTATTTCTTTCTCCGACGGGCCAGG 1439
QY      448 MetCysProGlyVal***LeuAlaThrSerGly***AlaThrLeuLeuAlaSerLeuIle 467
      1440 AACTGCATCGGAGAGCGCTTCCCATGCGGAGATGAAGATGTCCTGGGCTTGAATC 1499
QY      468 GlnCysPhe 470
      1500 CTGCACCTC 1508

```

RESULT 8
 US-11-000-463-641
 ; Sequence 641, Application US/11000463
 ; Publication No. US2005026423A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tang, Y. Tom
 ; APPLICANT: Liu, Chenghua
 ; APPLICANT: Asundi, Vinod
 ; APPLICANT: Chen, Rui-hong
 ; APPLICANT: Qian, Xiaohong B.
 ; APPLICANT: Wang, Zhiwei
 ; APPLICANT: Wehrman, Tom
 ; APPLICANT: Zhang, Jie
 ; APPLICANT: Zhou, Ping
 ; APPLICANT: Cao, Yi-Cheng
 ; APPLICANT: Drmanac, Radoje T.
 ; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
 ; FILE REFERENCE: 785CIPACN
 ; CURRENT APPLICATION NUMBER: US/11/000,463
 ; CURRENT FILING DATE: 2004-11-29
 ; PRIOR APPLICATION NUMBER: 10/291,265
 ; PRIOR FILING DATE: 2002-11-08
 ; PRIOR APPLICATION NUMBER: PCT/US01/02623
 ; PRIOR FILING DATE: 2001-01-25
 ; PRIOR APPLICATION NUMBER: 09/922,279
 ; PRIOR FILING DATE: 2001-08-03
 ; PRIOR APPLICATION NUMBER: 09/491,404
 ; PRIOR FILING DATE: 2000-01-25
 ; PRIOR APPLICATION NUMBER: 09/617,746
 ; PRIOR FILING DATE: 2000-07-17
 ; PRIOR APPLICATION NUMBER: 09/631,451
 ; PRIOR FILING DATE: 2000-08-03
 ; PRIOR APPLICATION NUMBER: 09/633,870


```

; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 641
; LENGTH: 1710
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-000-463-641

Alignment Scores:
Pred. No.:      8.15e-15      Length:      1710
Score:          190.00      Matches:      115
Percent Similarity: 34.03%      Conservative: 63
Best Local Similarity: 21.93%      Mismatches:  239
Query Match:      7.95%      Indels:      106
                        Gaps:      21

US-09-857-581b-66 (1-521) x US-11-000-463-641 (1-1710)

QY      1 MetLeuLeuGluLeuAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeuArgPro 20
      193 CTACTCTCTCTGCTGCTGTTGGGCTCTCGGCTACTCCG-----CGCATCTCGGCT 243
QY      21 ThrPro***Ala***SerLysAlaLeuArgHisLeuProAsnProProSerPro***Pro 40
      244 TGGACCTATGCTCTCTATTAACAACACTGCCGCGCTCCAGTGTTCACAGAGCCCAAAA 303
QY      41 ArgLeuProPheIleGlyHis***HisLeu-----LeuLysAsp 53
      304 CGGAAGCTGTTTGGGGTCACTGGGCTGATCACTCTCAAGAGAGGGCTTGAAGAC 363
QY      54 LysLeuLeuHisTyrAla***IleAspLeuSerLysHisGlyProLeuPheSer*** 73
      364 -----TGCACCCAGATGCGGCCACACTTATCCAGGGCTTTACGGTA 405
QY      74 ***PheGlySer---MetProThrValAlaIleSerThrProGluLeuPheLysLeuPhe 92
      406 TGGGTGGGTCCCATCATCCCTTCATGTTTATGCCACCTGACACCATCGGTCTATC 465
QY      93 LeuGln*****GluAla-----ThrSerPhe***ThrArgPheGlnThrSer 108
      466 ACCAATGCTCAGTGCATTCGACCCAGAGATATCTTTCATCAGGTTG----- 516
QY      109 Ala***Arg***LeuThrTyrAsp*****ValAla*****Pro----- 123
      517 -----CTGAAGCCCTGCTGGAGGAGG 540
QY      124 -----**GlyProTyrTyr***PheValArgLysLeuIleMetAsnAspLeu 139
      541 ATACTGCTGATGGGGGTGACAGTGGAGCGCCACCGTGGAGT-----CTG 588
QY      140 ***AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys*** 159
      589 ACGCCCGCTTCACATTCACATCTGAAAGTCTATATAAG---ATCTTCAACAAGAGT 645
QY      160 LeuArg***MetAlaGln-----**AlaGluAla***LysProLeuAsp 174
      646 GCAAAACATCATGCTTGACACAGTGGACAGCACTGGGCTAGAGGGCAGAGTGTCTGAC 705
QY      175 ***ThrGluGluLeuLeuLysTyr***AsnSerThr***SerMetMet***LeuGlyGlu 194
      706 ATGTTTGACACATC-----ACGCTCATGACCTTGGACAGT 741
QY      195 AlaGluGlu---IleArgAspIleAlaArgGluValLeuLysIle***GlyGluTyrSer 213
      742 CTACAGAAATGATCTTCAGCTTTGACGCCATTCAGAGAGAGCCAGTGAATATATT 801
QY      214 LeuThrAspPheIle***ProLeuLys***LeuLysValGlyLysTyrGluLysArgIle 233
      802 GCCACC-----ATTGTGAGCTCAGTGCCTT-----CTGAGAAAAGAGAC 843
QY      234 AspAspIleLeuAsnLysPheAsp----- 241

```

```

Db      844 CAGCATATCTCCACAGCATGAGCTTTCGTATTAACCTCTCCCATGAGCGGCGGCTTC 903
QY      242 -----ProValValGluArgValIleLysLysArgArg*** 253
Db      904 CACAGGGCTCGCGCTGTGTGATGATCTTACAGACGCTGATCATCGGAGGCGGCTCGC 963
QY      254 IleValArgArgArg***AsnGlyGlu*****GluGlyGlu***SerGlyVal***Leu 273
      964 ACCCTCCCATCTCAGGAGTATGATGATTTTTCATTAAGACAAAGCCAGTCCAAAGACTTGG 1023
QY      274 Asp-----ThrLeuLeuGluPheAlaGluAspGluThr***GluIleLysIleThrLys 291
      1024 GATTTATGATGATGCTGCTTCTGCTGAGCAAGATGAAGATGGAGAG---GCATTGTCAGAT 1080
QY      292 ****Ile***GlyLeuValValAsp***PheSerAlaGly***AspSerThrAla*** 311
      1081 GAGGATATTAAGACAGAGGCTGACACCTTCATGTTTGGAGCCATGACACAGCGGCAGT 1140
QY      312 ***ThrGluTyrAlaLeuAlaGluLeuIleAsnAsnPro***ValLeu*****AlaArg 331
      1141 GGCCTCTCTGCTGCTCTGTAACAACCTTGCAGAGGACCCAGAAATACAGAGCGCTGCCA 1200
QY      332 GluGlu***TyrSerValValGlyLysAsp***LeuValAspGluVal-----Asp 348
      1201 CAGAGAGTGCAGAGCTTCTG---AAGGACCGGATCTTAAGAGATGATGATGAGAGTAC 1257
QY      349 ThrGlnAsnLeuProTyrIleArgAlaIleValLysGluThrPheArgMetHisProPro 368
      1258 CTGGCCAGAGTGCCTTCTCTGACCATGTGGGTGAAGAGAGCTGATGATCATCCCCCA 1317
QY      369 LeuProValValLysArgLysCys***GluGluCys***Ile---AsnGly***Val*** 387
      1318 GCTCCCTTCATCTCCAGAGTCTGCACCCAGAGCATTTGTTCTCCAGATGGCCAGATCATC 1377
QY      388 ProGluGluValAlaLeu*****PheAsnValTyrGlnValGly***Asp***LysTyrTyr 407
      1378 CCAAAAGGCAATTTCCTGCTCATGATATTAAGGGTTCATACACCAACCACTGTGTGG 1437
QY      408 AspArgProSerGlu***ArgProGluArgPheLeuGluThr***AlaGluGlyGluAla 427
      1438 CCGATCTCTGAGGTCTACAGACCCCTCCGCTTGGACCCAGAGAAAGAGAGGAGAGTCA 1497
QY      428 ****LeuAspLeuArgGly***HisPheGlnLeuLeuProPheGlySerGlyArg*** 447
      1498 -----CCTCTGGCTTTATTAATCTTCTTCTCCGAGGCGCCAGG 1533
QY      448 MetCysProGlyVal***LeuAlaThrSerGly***AlaThrLeuLeuAlaSerLeuIle 467
      1534 AACTGCATCGGGGAGCGGCTTGCATAGCGGAGATGAAGTGGTCTGGCGTGTGATCTG 1593
QY      468 GlnCysPhe 470
      1594 CTGCACCTTC 1602

```

RESULT 9
 US-11-000-463-642
 : Sequence 642, Application US/11000463
 : Publication No. US20050266423A1
 : GENERAL INFORMATION:
 : APPLICANT: Tang, Y Tom
 : APPLICANT: Liu, Chenghua
 : APPLICANT: Asundi, Vinod
 : APPLICANT: Chen, Rui-hong
 : APPLICANT: Qian, Xiaohong B.
 : APPLICANT: Wang, Zhiwei
 : APPLICANT: Wehrman, Tom
 : APPLICANT: Zhang, Jie
 : APPLICANT: Zhou, Ping
 : APPLICANT: Cao, Yi-Cheng
 : APPLICANT: Drmanac, Radoje T.
 : TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
 : FILE REFERENCE: 785C1P4CN
 : CURRENT APPLICATION NUMBER: US/11/000,463

QY 448 MetCysProGlyVal***LeuAlaThrSerGly***AlaThrLeuAlaSerLeuIle 467
DB 1534 AACTGATGCGGAGCGCTTGGCCATGCGGAGATGAAGTGTCTGGCGTTGATGCTG 1593
QY 468 GlnCysPhe 470
DB 1594 CTGCACTTC 1602
RESULT 11
US-11-000-463-169
; Sequence 169, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radolje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIPACN
; CURRENT APPLICATION NUMBER: US/11/000,463
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 169
; LENGTH: 1906
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (108)..(1748)
; US-11-000-463-169
Alignment Scores:
Pred. No.: 2,45e-14 Length: 1906
Score: 187.00 Matches: 113
Percent Similarity: 34.68% Conservative: 67
Best Local Similarity: 21.77% Mismatches: 241
Query Match: 7.83% Indels: 98
DB: 7 Gaps: 21
US-09-857-581B-66 (1-521) x US-11-000-463-169 (1-1906)
QY 1 MetLeuLeuGluLeuAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeuArgPro 20
DB 231 CTACTCTGCTGCTGGTGTGGGCTCTGGCTACTGCC-----CCATCTCTGGCT 281
QY 21 ThrPro***Ala***SerLysAlaLeuArgHisLeuProAsnProProSerPro***Pro 40
DB 282 TGGACCTATGCGCTTTATTAACAACACTGCGCGGCTCGAGTGTTCACACAGCCCCCAAA 341
QY 41 ArgLeuProPheIleGlyHis***HisLeuLeu-----LysAspLysLeuLeuHis 57

DB 342 CGGAACGTGTTTGGGGTCACCTGGGCGCTGATCACTCTACAGAGAGGGCTTGAAGAAC 401
QY 58 TyrAla***IleAspLeuSerLysHisGlyProLeuPheSer*****PheGlySer 77
DB 402 TCGACCAAGATGTCGGCCACCTATTCCACAGGC-----TTTACATATGCTGGGTGCC 455
QY 78 ---MetProThrValValAlaSerThrProGluLeuPheLysLeuPheLeuGln***** 96
DB 456 ATCATCCCTTCATGCTTTATGCCACCTGACACCATCCGCTTATCAACATGCTCTCA 515
QY 97 GlnAla-----ThiSerPhe***ThrArgPheGlnThrSerAla***Arg*** 112
DB 516 GCTGCATTCGACCCCAAGGATATATCTTCATCAGGTTC----- 554
QY 113 LeuThrTyrAsp*****ValAla*****Pro----- 123
DB 555 -----CTGAAGCCCTGGCTGGAGAGAGGATACTGCTGAGT 590
QY 124 ***GlyProTyrTrp***PheValArgLysLeuIleMetAsnAspLeu***AsnAlaThr 143
DB 591 GCGGTGACAAGTGGAGCGGCCACCTCGGATG-----CTGAGCGCCGCTTC 638
QY 144 ThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***LeuArg***Met 163
DB 639 CATTTCAACATCCTGAAGTCTATATTAACG---ATCTTCAACAAGAGTCMAAACATCATG 695
QY 164 AlaGln-----**AlaGlnAla***LysProLeuAsp***ThrGluGlu 178
DB 696 CTTGACAAGTCGACGACCTGCGCTCAGAGGCGACGAGATGTCCTGAGCATGTTTGAGCAC 755
QY 179 LeuLeuLysTrp***AsnSerThr***SerMetMet***LeuGlyGlnAlaGluGln--- 197
DB 756 ATC-----ACCTCATGACCTTGACAGCTACAGAAATGC 791
QY 198 IleArgAspIleAlaArgLysValLeuLysIle***GlyGlyLysSerLeuThrAspPhe 217
DB 792 ATCTTCAGCTTGACAGCATTGTGCAGAGAGGCCAGCAAGAAATATATTGCCACCC----- 845
QY 218 Ile***ProLeuLys***LeuLysValGlyLysTyrGlnLysArgLysAspIleLeu 237
DB 846 ATCTTGAGACTCAGTGCCTT-----GTAGAGAAAAGAGCCAGCATATATCTC 893
QY 238 AsnLysPheAsp----- 241
DB 894 CAGCAATGAGCTTTGTGATTACCTCTCCCATGACGGGCGGCTTCCACAGGGCTGC 953
QY 242 -----ProValValGlnArgValIleLysLysArgArg***IleValArgArg 257
DB 954 CGCCTGTGCATGACTTCACAGACGCTGATCCGGAGCGGGCTGCACCCCTCCCACT 1013
QY 258 Arg***AsnGlyGlu*****GluGlyGlu***SerGlyVal***LeuAsp-----Thr 275
DB 1014 CAGGTAATTGATGATTTTTCAAAGACAAGCCAAAGCTCAAGACTTGTGATTTCATGAT 1073
QY 276 LeuLeuGluPheAlaGluAspGluThr***GluIleLysIleThrLys*****Ile*** 295
DB 1074 GTGCTTCTGTGACAGAGATGAAGTGGAGG---GCATGTGCATAGATAGATATTAAGA 1130
QY 296 GlyLeuValValAsp***PheSerAlaGly***AspSerThrAla*****ThrGluTrp 315
DB 1131 GCAGAGGTGACACCTTCATGTTTGAGGCGCATGACACACGCGCAGTGCCTCTCTCG 1190
QY 316 AlaLeuAlaGluLeuIleAsnAsnPro***ValLeu*****AlaArgGluGlu***Tyr 335
DB 1191 GTCTCTTACAACTTTCGAGGACCCAGAAATACACAGACGCTGCGACAGAGGTGCAC 1250
QY 336 SerValValGlyLysAsp***LeuValAspGluVal-----AspThrGlnAsnLeu 352
DB 1251 GAGCTTCTG---AAGAGCCGCGATCTTAAGAGATTTGAGGACAGACCTGGCCCAAGCTG 1307
QY 353 ProTyrIleArgAlaIleValLysGluThrPheArgMetHisProProLeuProValVal 372

Db 1308 CCCTTCCTGACATGTCGTGAAGAGAGCTGATTCATCCCGAGCTCCCTTCATC 1367
Qy 373 LysArgLysCys***GluGluCys***Ile---AsnGly***Val***ProGluGlyAla 391
Db 1368 TCCCGATGCTGCACCCAGCATGTTCTTCCCAAGATGCGCATCCCAAGGCAATT 1427
Qy 392 Leu*****PheAsnValTrrpGluValGly***Asp***LysTrrpAspArgProSer 411
Db 1428 ACCTGCTCATGATATTAATAGGGGTTCATCACACCAACTGTGTGCGCGATCCGTAG 1487
Qy 412 Glu***ArgProGluArgPheLeuGluThr***AlaGluGlyGluAla*****LeuAsp 431
Db 1488 GTCACAGACCCCTTCCGCTTGAACCCAGAGACGCAAGGAGGTCA----- 1535
Qy 432 LeuArgGly***HisPheGlnLeuLeuProPheGlySerGlyArg***MetCysProGly 451
Db 1536 -----CCTGTGGCTTTTATTCTTCTCCGAGGGCCCGAGAACTGCATCGGG 1583
Qy 452 Val***LeuAlaThrSerGly***AlaThrLeuLeuAlaSerLeuLeuGlnCysPhe 470
Db 1584 CAGCGCTTCGCCATGCGGAGATGAAGTGTCTCTGCTGATGCTGTGCACTTC 1640
RESULT 12
US-10-507-106-1
; Sequence 1, Application US/10507106
; Publication No. US20050246797A1
; GENERAL INFORMATION:
; APPLICANT: Japan Science and Technology Agency
; TITLE OF INVENTION: Gene participating in the synthesis of brassinosteroid
; FILE REFERENCE: 26352U (P803-311PCT)
; CURRENT APPLICATION NUMBER: US/10/507,106
; CURRENT FILING DATE: 2004-09-10
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1473
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-507-106-1
Alignment Scores:
Pred. No.: 1.96e-14 Length: 1473
Score: 186.50 Matches: 101
Percent Similarity: 35.81% Conservative: 77
Best Local Similarity: 20.32% Mismatches: 214
Query Match: 7.81% Indels: 105
Gaps: 17
US-09-857-581b-66 (1-521) x US-10-507-106-1 (1-1473)
Qy 18 LeuArgProThrPro***Ala***SerIleAlaLeuArgHisLeuProAsnProProSer 37
Db 79 CTCGATCATCTCCAGCTTCAAGAAAACTTAATGATCATCATGTTATCCCAAGAT 138
Qy 38 Pro***ProArgLeuPro----- 43
Db 139 CACGAGCAAGTTTCCACAGGAAGCTTGGATGCGCCGTCATCGGTGAACCATGAG 198
Qy 44 PheIleGlyHis***His-----LeuLeuLysAspLysLeuLeu 56
Db 199 TTCGCTCTTCTGCTTACTCAGACCGTCCTGAGAGTTTCATGACACACGTCGCTCATG 258
Qy 57 HisIleAla***IleAspLeuSerLysHisGlyProLeuPheSer*****PheGly 76
Db 259 -----TATGGAGAGGTGTTTAAGTCGATATTTT 288
Qy 77 SerMetProThrValAlaSerThrProGluLeuPheLysLeuPheLeuGln***** 96
Db 289 GGAAGCGGAGCATGTGTGCGATGCTGTAAGTGAACAGCGGTTTACAG---AGC 345
Qy 97 GluAlaThrSerPhe***ThrArgPheGlnThrSerAla***Arg***LeuThrLysAsp 116
Db 346 GACTCGACAGCTTTC---GTGCGGTTTAAACCAAAAACGTAAGGAGCTAATGGGAAA 402

Qy 117 *****ValAla*****Pro***GlyProLysTrrp***Phe-----ValArgLys 133
Db 403 TCGTCGATCTCTTATCAACCGAGATTATTAAGCGGTTCATGATGATGATGCTGCT 462
Qy 134 LeuIleMetAsnAspLeu***AsnAlaThrThrValAsn***Leu----- 148
Db 463 TTTCTTAAGTCCCACTTCTCAAGCTCAATTCGTTAGACATGACACAAGTTTGTGCG 522
Qy 149 -----ArgProLeuArgThrGlnGlnIleArgLys*** 159
Db 523 GAATCATGATGATATGTCGCGAGACCAACTGTGCTCTCCACAGACGCTCCAGACT 582
Qy 160 LeuArg***MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGluGluLeu 179
Db 583 GTT-----GCATTCAAAGTACT----- 600
Qy 180 LeuLysTrrp***AsnSerThr***SerMetMet***LeuGlyGluAlaGluGluIleArg 199
Db 601 -----GCCAAGCATGATTAAGTGTGAGAAAGAGAAAGATTGAA 642
Qy 200 AspIleAlaArgGluValLeuLysIle***GlyGluTrrpSerLeuThrAspPheIle*** 219
Db 643 GACTTAAGAGAGAG-----TTTGAAATTCATATCA 675
Qy 220 ProLeuLys***LeuLysVal-----GlyLysTrrpGluLysArgIleAspIle 236
Db 676 GACTCATGATCATTAACCAATTAACTCCCTGGAACCAATCCATGATCTCCAGACT 735
Qy 237 LeuAsnLysPheAspProValValGluArgValIleLysLysArgArg***IleValArg 256
Db 736 AAGAGAAATATGCTGAGCAAGTGAAGATATGAAGGCAAA-----ATTAGG 786
Qy 257 ArgArg***AsnGlyGlu***GluGlyGlu***SerGlyVal***LeuAspThrLeu 276
Db 787 AAAACAAGAACAAAGAGAGAGATGATGTTATTCGAAAGATTT---GTGATGTGCTG 843
Qy 277 LeuGluPheAlaGluAspGluThr***GluIleLysIleThrLys*****Ile***Gly 296
Db 844 CTTAAGGACTCAAGTGAACAT-----TTAATCTCAATTTGATTTGCTTAC 888
Qy 297 LeuValValAsp***PheSerAlaGly***AspSerThrAla*****ThrGluTrrpAla 316
Db 889 AATATGATCAACATGATGATCCTGCGCAGATTCGTCTGCTCATTAACCTTGCC 948
Qy 317 LeuAlaGluLeuIleAsnAsnPro***ValLeu*****AlaArgGluGlu***TyrSer 336
Db 949 GTCAAAATCTCTCTGATTTCTCTGCTGCGCCCTCATCTCCTAAGAAAACATGAAGCTG 1008
Qy 337 ValValGlyLysAsp***LeuValAspGluVal-----AspThrGlnAsnLeuPro 353
Db 1009 AAAAGTTTGAAGGAATTGACAGAGAGCCACTATATTGATGATCATCTTGTGTTACCT 1068
Qy 354 TyrIleArgAlaIleValLysGluThrPheArgMetHisProProLeuProValValLys 373
Db 1069 TTAACACAAAAGGATTACAGAGACCTGAGATGGAAAATGTTAATTTGAGATGATG 1128
Qy 374 ArgLysCys***GluGluCys***IleAsnGly***Val***ProGluGlyAlaLeu*** 393
Db 1129 AGAAGCGCATGAAGATGTTGAATTAAGATATGATATACCAAAAGATGTGTTTC 1188
Qy 394 ***PheAsnValTrrpGluValGly***Asp***LysTrrpAspArgProSerGlu*** 413
Db 1189 TTGGCTATCTCAGATCAGTTATCTCTGATGAAGACTTATATGATGCTCGTACAAATTT 1248
Qy 414 ArgProGluArgPheLeuGluThr***AlaGluGlyGluAla*****LeuAspLeuArg 433
Db 1249 AATCCCTGAGATGCAAGAAAG-----GACATGAC 1281
Qy 434 Gly***HisPheGlnLeuLeuProPheGlySerGlyArg***MetCysProGlyVal*** 453
Db 1282 ACGAGTATGTTCACT-----CTTTTGAGAGTGTGACAGATATGTCCTCGTCTGAT 1335


```

Db      1378 CTCGCCAAGTAAATTTTATATTTCTCCACATTAGTTTCCATTTCGATGGAA 1437
QY      474 ValLeuGlyProGlnGlyGlnIleLeuGly***AspAlaIysValSerMetGluGlu 493
Db      1438 GTCAAGGAGAGAGAG-----AAAGAAATACAGTACGATCCATTTCGAATACCT 1485
QY      494 ArgAlaGlyLeuThrValPro---ArgAlaHisSerLeu 505
Db      1486 CAAAACGCTCTCCCGCTACATTTCGTGCACATTCTCTT 1524

RESULT 15
US-10-995-561-81
; Sequence 81, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILE, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81
; LENGTH: 2361
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-81

Alignment Scores:
Pred. No.:      3e-13      Length:      2361
Score:          180.00     Matches:      104
Percent Similarity: 34.38%   Conservative: 71
Best Local Similarity: 20.43% Mismatch:      211
Query Match:      7.53%     Gaps:         20
DB:              6

US-09-857-581b-66 (1-521) x US-10-995-561-81 (1-2361)
QY      20 ProThrPro***Ala***SerLysAlaLeuArgHisLeuProAsnProProSerPro*** 39
Db      147 CCATGTCCTGGCTGAGCTGACCTGCTTATGACAACTGCG--CCGCTTCGGTGT 203
QY      40 ProArgLeuProPheIle-----GlyHis***HisLeuLeu 52
Db      204 CCCAACACCCCCAGACGGAACCTGTTGGGACACCCAGGCAATGATTCACAGCTCAGA 263
QY      52 SAAPLysLeuLeuHisIleTyAla***IleAspLeuSerLysLysIleGlyProLeuPhe 72
Db      264 AGAAGCTCTCTTATACACAAAGCCTG-----GC 293
QY      72 r*****PheGlySerMet----- 78
Db      294 GTGCACCTTTGGGGATATGGGCTGCTGGTGGGGCCCTGAGCAGCAGTCAATCCACAT 353
QY      79 -----ProThrValValAlaSerThrPr 86
Db      354 CTTTCTCCCAAGCTGATCAAGCTGTGCTCTTTGCTCCAGCTGCCATGACCAAGAA 413
QY      86 ogLysLeuPheLysLeuPheLeuGln*****GluAlaThrSerPhe***ThrArgPheG 106
Db      414 CAAGTTTCTTACAGCTTCTCGAGCCCTGGCTGGGGATGGGCTC----- 459
QY      106 nThrSerAla***Arg***LeuThrTyArgPhe***ValAla*****Pro***GlyPr 126
Db      460 -----CTGCTGAGTGGCTGCTGA 476
QY      126 oTyTrp***PheValArgLysLeuIleMetAsnAspLeu***AsnAlaThrThrValAs 146
Db      477 CAAGTGAGCCRCACACGCTGGAGT-----CTGACGCTGCTCTTCATTTCA 524
QY      146 n***LeuArgPro-----LeuArgThrGlnGlnIleArg---Lys***LeuArg** 162

```

```

Db      525 CATCTGAAGCCCTATATGATGATTTTCAATGAGAGTGTGAACATCATGCACGCCAAGTG 584
QY      162 *MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGlnGlnLeuLysTr 182
Db      585 GCAGCTCTGGCTCCAGAGDPAATGCTCTTTGGATATGTTTGAACACATC----- 636
QY      182 p***AasnSerThr***SerMetMet***LeuGlyGluAlaGluGlu----- 197
Db      637 -----AGCTCATGACCTTGACACGTCTACAGAAATGTGTCTTCAGCTT 680
QY      198 -----IleArgAspIleAlaAr 203
Db      681 TGACACGCAATGTGACAGAGAAACCAGTGAATATATTGCCGCACTTGAGAGCTGATGC 740
QY      203 gGluValLeuLysIle***GlyGlyTrpSerLeu---ThrAspPheIle***ProLeu 222
Db      741 CTTGTATCAAAAAGACACCATGAGATCTCTGCTGATATGACTTCTGTATTTATCTC-- 798
QY      222 s***LeuLysValGlyLysTyrgLysArgIleAspAspIleLeuAsnLysPheAspPr 242
Db      799 -----ACCCCTGATGGCAGCGTTCCGACAGGCTGCCCTGTGTGCACAGACTTC----- 849
QY      242 oValValGluArgValIleLysLysArgArg***IleValArgArgArg***AsnGly 262
Db      850 ---ACAGATGCCGTCATCCAGAGCGCGCCGCACTCTCCCTAGCCAGAGTTTGATGA 905
QY      262 u*****GluGlyGlu***SerGlyVal***LeuAsp-----ThrLeuLeuGluPheAl 280
Db      906 CTTCTCCCAAGCCCAACCAATCCAGACTTTGACCTTCATGATGATGACTCTGCTGAG 965
QY      280 agLysArgLysThr***GluIleLysIleThrLys*****Ile***GlyLeuValValAs 300
Db      966 CAGAGTAAAGACGGGAAG---AAGTTATCTGATGAGCATATAGACGAAGAGCTGACAC 1022
QY      300 p***PheSerAlaGly***AspSerThrAla*****ThrGlyTrpAlaLeuAlaGlu 320
Db      1023 CTTTATGTTGAGGGCCATGACACACGCGCAGTGTCTCTCCGCGTCTGTACCACT 1082
QY      320 uIleAsnAsnPro***ValLeu*****AlaArgGlnGlu***TyrSerValValGlyLys 340
Db      1083 TGCAAAGCACCCCAAGATATACAGAGCGCTGCGCAGAGAGTGCAGAAACTTGTG--AA 1139
QY      340 SAAP***LeuValAspGluVal-----AspThrGlnAsnLeuProTyrlIleArgAl 357
Db      1140 GGAACGCGTGAACCTTAAGAGATTTGAATGAGACGACCTGGCCATTTCCCTCTGACCAAT 1199
QY      357 aIleValLysGlyThrPheArgMetHisProProLeuProValValLysArgLysCys** 377
Db      1200 GTGCATGAAGAGAGAGCTGGCGCTGCATCCCAAGTCCCGGTCACTCCCGCATGTCAAC 1259
QY      377 *GluGlyCys***Ile---AsnGly***Val***ProGlnGlyValLeu*****PheAs 396
Db      1260 CCAGACATTTGTGCTCCAGACGCGCGGTGCATCCCAAGGATATATCTGCTCATACAG 1319
QY      396 nValTrpGlnValGly***Asp***LysTyrlTrpAspArgProSerGluu***ArgProG 416
Db      1320 TGTTTTCGAACCAACATCACACACCACTGTGTGCGGACCCCTGAGAGTCTACGACCCCTT 1379
QY      416 uArgPhe---LeuGluThr***AlaGlnGlyGluAla*****LeuAspLeuArgGly** 435
Db      1380 TCGCTTTGACCCAGAGAACATCAAGAGAGAGTCACT----- 1416
QY      435 *HisPheGlnLeuLeuProPheLysArgLysArg***MetCysPProGlyVal***LeuAl 455
Db      1417 ---CTGGCTTTTATTTCTTCTCGGCAAGGCCCAAGAACTGATCGGGACAGCTTCCG 1472
QY      455 aThrSerGly***AlaThrLeuLeu 463
Db      1473 GATGCGGAGATGAAGTGTCTCTG 1497

```


Fri Dec 23 08:58:15 2005

us-09-857-581b-66.rnpbn

Page 17

Job time : 317 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 21, 2005, 21:08:13 (Search time 45 Seconds
(without alignments)
957.201 Million cell updates/sec

Title: US-09-857-581b-66

Perfect score: 2389
Sequence: 1 MLELALGLVIALFXHLRP.....ASHLVCPILARIGVASKILS 521

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PCrus_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------------|
| 1 | 2250 | 94.2 | 521 | 2 | US-08-948-564-14 |
| 2 | 944.5 | 39.5 | 512 | 2 | US-09-672-785-4 |
| 3 | 940.5 | 39.4 | 506 | 2 | US-09-672-785-2 |
| 4 | 921.5 | 38.6 | 506 | 2 | US-09-672-785-8 |
| 5 | 651 | 27.2 | 513 | 2 | US-09-351-229-4 |
| 6 | 637.5 | 26.7 | 508 | 2 | US-09-142-108C-17 |
| 7 | 629 | 26.3 | 495 | 2 | US-09-688-783A-2 |
| 8 | 626 | 26.2 | 512 | 2 | US-09-142-108C-6 |
| 9 | 623 | 26.1 | 513 | 2 | US-09-142-108C-15 |
| 10 | 618.5 | 25.9 | 496 | 2 | US-09-292-768-2 |
| 11 | 618.5 | 25.9 | 496 | 2 | US-09-292-768-66 |
| 12 | 615 | 25.8 | 496 | 2 | US-08-881-784-1 |
| 13 | 615 | 25.8 | 500 | 2 | US-09-292-768-4 |
| 14 | 615 | 25.8 | 500 | 2 | US-09-292-768-68 |
| 15 | 615 | 25.8 | 512 | 2 | US-09-142-108C-2 |
| 16 | 615 | 25.8 | 500 | 2 | US-09-292-768-70 |
| 17 | 613.5 | 25.7 | 496 | 2 | US-09-292-768-64 |
| 18 | 613.5 | 25.7 | 500 | 2 | US-08-881-784-9 |
| 19 | 608 | 25.4 | 502 | 2 | US-09-499-302A-2 |
| 20 | 606.5 | 25.4 | 496 | 2 | US-09-172-335-6 |
| 21 | 602.5 | 25.2 | 471 | 2 | US-09-126-420A-20 |
| 22 | 599.5 | 25.1 | 498 | 2 | US-09-292-768-6 |
| 23 | 592 | 24.8 | 508 | 2 | US-09-142-108C-19 |
| 24 | 590.5 | 24.7 | 500 | 2 | US-09-142-108C-4 |
| 25 | 590 | 24.7 | 517 | 2 | US-09-142-108C-21 |
| 26 | 583 | 24.4 | 516 | 2 | US-08-948-564-12 |
| 27 | 574 | 24.0 | 496 | 1 | US-08-313-075A-50 |

ALIGNMENTS

| | | | | | | |
|----|-------|------|-----|---|--------------------|-------------------|
| 28 | 574 | 24.0 | 496 | 2 | US-09-142-108C-41 | Sequence 41, Appl |
| 29 | 572 | 23.9 | 502 | 2 | US-09-499-302A-4 | Sequence 4, Appl |
| 30 | 570.5 | 23.9 | 510 | 2 | US-08-606-505B-66 | Sequence 66, Appl |
| 31 | 570.5 | 23.9 | 510 | 2 | US-09-616-990-66 | Sequence 66, Appl |
| 32 | 567 | 23.7 | 476 | 2 | US-09-142-108C-23 | Sequence 23, Appl |
| 33 | 566.5 | 23.7 | 476 | 1 | US-08-313-075A-30 | Sequence 30, Appl |
| 34 | 564 | 23.6 | 523 | 2 | US-08-606-505B-67 | Sequence 67, Appl |
| 35 | 564 | 23.6 | 523 | 2 | US-09-616-990-67 | Sequence 67, Appl |
| 36 | 563.5 | 23.6 | 506 | 1 | US-08-313-075A-38 | Sequence 38, Appl |
| 37 | 563.5 | 23.6 | 506 | 2 | US-08-606-505B-65 | Sequence 65, Appl |
| 38 | 563.5 | 23.6 | 506 | 2 | US-09-616-990-65 | Sequence 65, Appl |
| 39 | 562.5 | 23.5 | 513 | 2 | US-09-142-108C-42 | Sequence 42, Appl |
| 40 | 561.5 | 23.5 | 514 | 2 | US-09-947-027-4 | Sequence 4, Appl |
| 41 | 559.5 | 23.4 | 529 | 2 | US-09-615-192A-405 | Sequence 405, App |
| 42 | 556.5 | 23.3 | 490 | 2 | US-09-126-420A-16 | Sequence 16, Appl |
| 43 | 556.5 | 23.3 | 520 | 1 | US-09-091-432-2 | Sequence 2, Appl |
| 44 | 556.5 | 23.3 | 520 | 2 | US-09-387-663-2 | Sequence 2, Appl |
| 45 | 556.5 | 23.3 | 520 | 2 | US-09-214-139B-4 | Sequence 4, Appl |

RESULT 1
US-08-948-564-14
Sequence 14, Application US/08948564

Patent No. 6121512
GENERAL INFORMATION:
APPLICANT: Siminszky, Balazs
APPLICANT: Dewey, Ralph E.
APPLICANT: Corbin, Frederick T.
TITLE OF INVENTION: No. 6121512 Cytochrome P-450 Constructs and
TITLE OF INVENTION: Methods of Producing Herbicide-Resistant Transgenic Plants
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Virginia C. Bennett
STREET: PO Box 37428
CITY: Raleigh
STATE: No. 6121512th Carolina
COUNTRY: USA
ZIP: 27627

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/948,564
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Virginia C.
REGISTRATION NUMBER: 37,092
REFERENCE/DOCKET NUMBER: 5051-409
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-854-1401
TELEFAX: 919-854-1400
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 521 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-948-564-14

Query Match 94.2% Score 2250; DB 2; Length 521;
Best Local Similarity 86.6%; Pred. No. 2.3e-273;
Matches 451; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

Qy 1 MLELALGLVIALFXHLRPTXAXSKALRHLPNPPSPXPLPTIGHXHLKDKILHYAX 60
Db 1 MLELALGLVIALFXHLRPTXAXSKALRHLPNPPSPXPLPTIGHXHLKDKILHYAL 60

| | | | |
|----|-----|--|-----|
| Qy | 61 | DL\$KXHGFLFX\$XFGSMPTVA\$TE\$FLFLOX\$X\$E\$FXFRFC\$X\$X\$X\$LYDXVA | 120 |
| Dd | 61 | IDL\$KXHGFLFX\$XFGSMPTVA\$TE\$FLFLOX\$X\$E\$FXFRFC\$X\$X\$X\$LYDXVA | 120 |
| Qy | 121 | XXPK\$GYMX\$V\$KRL\$MNDL\$XNAT\$V\$X\$X\$LP\$LT\$OQIR\$K\$X\$X\$MA\$Q\$X\$E\$X\$K\$P\$LDX\$TE\$LL | 180 |
| Dd | 121 | M\$P\$F\$P\$Y\$M\$F\$V\$K\$RL\$MNDL\$P\$N\$AT\$V\$X\$X\$LP\$LT\$OQIR\$K\$F\$R\$V\$X\$V\$A\$O\$G\$E\$A\$O\$K\$P\$LDL\$TE\$LL | 180 |
| Qy | 181 | K\$M\$N\$T\$X\$S\$M\$X\$X\$G\$E\$A\$E\$I\$R\$D\$I\$A\$R\$E\$V\$X\$K\$I\$G\$E\$Y\$L\$T\$D\$F\$I\$P\$K\$X\$K\$X\$K\$Y\$G\$E\$K\$R\$I\$D\$D\$I\$N\$K\$F | 240 |
| Dd | 181 | K\$M\$N\$T\$I\$S\$M\$M\$M\$G\$E\$A\$E\$I\$R\$D\$I\$A\$R\$E\$V\$X\$K\$I\$G\$E\$Y\$S\$L\$T\$D\$F\$I\$M\$P\$L\$K\$X\$K\$X\$G\$E\$K\$R\$I\$D\$D\$I\$N\$K\$F | 240 |
| Qy | 241 | D\$P\$V\$R\$V\$R\$V\$I\$K\$R\$R\$X\$I\$Y\$R\$R\$R\$X\$N\$G\$E\$X\$E\$G\$S\$G\$V\$X\$LDL\$T\$LE\$F\$A\$D\$E\$T\$X\$E\$I\$K\$I\$T\$K\$X\$X\$I\$G\$L\$V\$D | 300 |
| Dd | 241 | D\$P\$V\$R\$E\$V\$I\$K\$R\$R\$E\$I\$Y\$R\$R\$R\$K\$N\$G\$E\$V\$E\$B\$E\$S\$G\$V\$P\$LDL\$T\$LE\$F\$A\$D\$E\$T\$M\$E\$I\$K\$I\$K\$O\$H\$I\$E\$G\$L\$V\$D | 300 |
| Qy | 301 | X\$F\$S\$A\$G\$X\$D\$T\$A\$X\$X\$T\$E\$M\$A\$L\$E\$I\$N\$N\$P\$X\$Y\$L\$X\$A\$R\$E\$X\$Y\$S\$Y\$V\$G\$D\$X\$Y\$D\$E\$V\$T\$O\$N\$L\$P\$I\$Y\$R\$A\$I\$Y\$K | 360 |
| Dd | 301 | P\$F\$S\$A\$G\$T\$D\$S\$T\$A\$V\$A\$T\$E\$M\$A\$L\$E\$I\$N\$N\$P\$K\$Y\$L\$E\$K\$A\$R\$E\$E\$V\$Y\$S\$V\$G\$D\$R\$Y\$D\$E\$V\$T\$O\$N\$L\$P\$I\$Y\$R\$A\$I\$Y\$K | 360 |
| Qy | 361 | E\$F\$F\$R\$H\$P\$P\$L\$Y\$V\$Y\$R\$K\$C\$E\$B\$X\$X\$I\$N\$G\$X\$Y\$X\$P\$E\$G\$A\$L\$X\$X\$F\$N\$W\$O\$Y\$G\$X\$D\$X\$K\$Y\$D\$R\$E\$S\$E\$K\$P\$E\$R\$F\$LE | 420 |
| Dd | 361 | E\$T\$F\$R\$H\$P\$P\$L\$Y\$V\$Y\$R\$K\$K\$T\$E\$B\$C\$E\$I\$N\$G\$Y\$I\$P\$E\$B\$A\$L\$L\$F\$N\$W\$O\$Y\$G\$R\$D\$K\$Y\$D\$R\$E\$S\$E\$P\$E\$R\$F\$LE | 420 |
| Qy | 421 | T\$Y\$A\$E\$G\$E\$A\$X\$X\$L\$D\$R\$G\$X\$H\$F\$O\$L\$L\$P\$E\$G\$S\$G\$X\$M\$C\$P\$G\$V\$X\$L\$A\$T\$S\$G\$A\$T\$L\$L\$A\$S\$L\$I\$Q\$C\$F\$D\$L\$O\$Y\$L\$G\$P\$O\$Q | 480 |
| Dd | 421 | T\$O\$A\$E\$G\$E\$A\$G\$E\$L\$D\$R\$G\$H\$F\$O\$L\$L\$P\$E\$F\$S\$G\$R\$M\$C\$P\$G\$V\$N\$L\$A\$T\$S\$G\$M\$A\$T\$L\$L\$A\$S\$L\$I\$Q\$C\$E\$D\$L\$O\$Y\$L\$G\$P\$O\$Q | 480 |
| Qy | 481 | I\$K\$G\$D\$A\$K\$Y\$S\$M\$E\$R\$A\$G\$L\$T\$V\$P\$R\$A\$S\$I\$Y\$C\$V\$P\$L\$A\$R\$I\$G\$V\$S\$K\$L\$S | 521 |
| Dd | 481 | I\$K\$G\$D\$A\$K\$Y\$S\$M\$E\$R\$A\$G\$L\$T\$V\$P\$R\$A\$S\$I\$Y\$C\$V\$P\$L\$A\$R\$I\$G\$V\$S\$K\$L\$S | 521 |

```

1      RESULT 2
2      US-09-672-785-4
3      ; Sequence 4, Application US/09672785
4      ; Patent No. 6596927
5      ; GENERAL INFORMATION:
6      ; APPLICANT: Mizutani, Masako
7      ; APPLICANT: Kaesumi, Takaaki
8      ; APPLICANT: Ayabe, Shin-ichi
9      ; APPLICANT: Akashi, Tomoyoshi
10     ; TITLE OR INVENTION: Genes Coding for Flavone Synthases
11     ; FILE REFERENCE: 001560-383
12     ; CURRENT APPLICATION NUMBER: US/09/672,785
13     ; CURRENT FILING DATE: 2000-09-29
14     ; PRIOR APPLICATION NUMBER: PCT/JP00/04379
15     ; PRIOR FILING DATE: 2000-01-30
16     ; PRIOR APPLICATION NUMBER: PCT/JP00/00490
17     ; PRIOR FILING DATE: 1999-01-28
18     ; PRIOR APPLICATION NUMBER: JP 11-205229
19     ; PRIOR FILING DATE: 1999-01-19
20     ; PRIOR APPLICATION NUMBER: JP 11-22427
21     ; PRIOR FILING DATE: 1999-01-29
22     ; NUMBER OF SEQ ID NOS: 8
23     ; SOFTWARE: PatentIn version 3.0
24     ; SEQ ID NO 4
25     ; LENGTH: 512
26     ; TYPE: PRT
27     ; ORGANISM: Torenia hybrida
28     ; FEATURE:
29     ; OTHER INFORMATION: Amino acid sequence of a protein having an activity to
30     ; OTHER INFORMATION: directly convert Flavonone to Flavone
31     US-09-672-785-4

```

| | | | | | | | |
|-----------------------|-------|--------------|----------|------------|-----|--------|-----|
| Query Match | 5% | Score | 944.5 | DB | 2 | Length | 512 |
| Best Local Similarity | 38.9% | Pred. No. | 2,1e-109 | | | | |
| Matches | 193 | Conservative | 94 | Mismatches | 182 | Indels | 27 |
| Gaps | | | | | | | 8 |

| | | | |
|----|----|---|----|
| QY | 33 | PNPDSXKPLPTFGKXHLKDKILMAYAXIDLSKGGPFLSSXFGSNPTVASTPEFLKFL | 92 |
| DB | 29 | PSPPGGL-SLPTTGHMLLGPRL-LHTTFEFSLSKGPPLQLQIKSGISLPCVASTPELAREF | 86 |

```

QY 93 :OXXEATSPFXRFOFSARXLYLVDXXVXXXPGXGYWXFVRKLIIMDLXNATVYNXLRPLR 152
Db 87 LKTNE-LAFSSRKSHALDIYVYDSSFAFSFGPIYWKYIKKLCYTEYLLGARNLGHQPIR 145
QY 153 TQOIRKXLRMAOXAAXKPLDYTEELLKWNXSTYSMMXL-----GEAEFIIDARE 204
Db 146 NLEVASFLQILMHKSPKSGSVNATDELVLNTSNVLSHMLSLRCSDEBDPAEAARVIRE 205
QY 205 VLKIXGEYSLDPEFIKPLKXKXKEKRIDDLINKFPDVERIYKRRXIVRRRXNGEXX 264
Db 206 VTQIRGEFDVDDIIMFCKKFDLOGIKKSEDIQRDYALLEKISRER-SRRQRDKH 263
QY 265 BG---EXSGVXLDTLLEFADETXEIKIYKXXIXGLVDXFSAKXDSTAXTEWALAEI 321
Db 264 GGGNNBEAKDPLDMLLDVWESGDTEVKKFRBHLKALILDFFTAGTDTTAAIATEWALAEI 323
QY 322 NNPFYLLXAXREXSVSGKDXLVDEVDTONLYIARIVKETPRMHPLPVVRKKCEBX 381
Db 324 NNPNVLKKAQBEISRIIGTKRIVQESDADPLQIYIKETFLPHPIPLSKKSTSDCT 383
QY 382 INGVXYPGALATXXFVVWQVQXGDKXKWDRESEKRPERFLETXAEGAXXXLDLRGXHQLP 441
Db 384 VNGVYIKQAKSLFLVNIWMSGRNPNVWESPMERPERFLEKGR-----SIDVQGHFELP 439
QY 442 FSGGKXMCBGVYLATISGAXTLIASLIQCPDLOYLGRQOQILKGDAXKVSNEEBAAGLTVPR 501
Db 440 FGTGRRGCGMMLIAQEVVSIIGTWQCPD-----WKLADSGNNVMDTERTSGLTAPR 492
QY 502 AHSIVCPLARIIGVAS 517
Db 493 AFDVLCRLYRPDPAF 508

```

```

    RESULT 3
    US-09-672-785-2
    ; Sequence 2, Application US/09672785
    ; Patent No. 6596927
    ; GENERAL INFORMATION:
    ; APPLICANT: Mizutani, Masako
    ; APPLICANT: Kasumi, Takaaki
    ; APPLICANT: Ayabe, Shin-ichi
    ; APPLICANT: Akashi, Tomoyoshi
    ; TITLE OF INVENTION: Gene Coding for Flavone Synthases
    ; FILE REFERENCE: 001560-383
    ; CURRENT APPLICATION NUMBER: US/09/672,785
    ; CURRENT FILING DATE: 2000-09-29
    ; PRIOR APPLICATION NUMBER: PCT/JP00/04379
    ; PRIOR FILING DATE: 2000-01-30
    ; PRIOR APPLICATION NUMBER: PCT/JP00/00490
    ; PRIOR FILING DATE: 1999-01-28
    ; PRIOR APPLICATION NUMBER: JP 11-205229
    ; PRIOR FILING DATE: 1999-01-19
    ; PRIOR APPLICATION NUMBER: JP 11-22427
    ; PRIOR FILING DATE: 1999-01-29
    ; NUMBER OF SEQ ID NOS: 8
    ; SOFTWARE: PatentIn version 3.0
    ; SEQ ID NO 2
    ; LENGTH: 506
    ; TYPE: PRT
    ; ORGANISM: Antirrhinum majus
    ; FEATURE:
    ; OTHER INFORMATION: Amino acid sequence of a protein having an activity to
    ; OTHER INFORMATION: directly convert flavanone to flavone
    US-09-672-785-2
  
```

| | | | | |
|-----------------------|-------|--------------------|------|-----------------------------------|
| Query Match | 39.4% | Score 940.5 | DB 2 | length 506 |
| Best Local Similarity | 39.8% | Pred. NO. 6.7e-109 | | |
| Matches | 196 | Conservative | 86 | Mismatches 185; Indels 25; Gaps 9 |

| | | | |
|----|----|--|----|
| QY | 30 | RILNPSPSPRLPRTGKXHLIKDKLLIYAYKIDLSKKRGPLESSXFFSGMPPTVASTPELF | 89 |
| DB | 24 | RKRTPPGGL-ALPIGHIHLGLGF-LHTTFHQFSQRQRLQQLYLVSPCCVASTPEIA | 81 |

[illegible]

RESULT 4
US-09-672-785-8
; Sequence 8, Application US/09672785
; Patent No. 6596927
; GENERAL INFORMATION:
; APPLICANT: Mizutani, Masaoko
; APPLICANT: Kaumli, Takaki
; APPLICANT: Ayabe, Shin-ichi
; APPLICANT: Akashi, Tomoyoshi
; TITLE OF INVENTION: Genes Coding for Flavone Synthases
; FILE REFERENCE: 001560-383
; CURRENT APPLICATION NUMBER: US/09/672,785
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JP00/04379
; PRIOR FILING DATE: 2000-01-30
; PRIOR APPLICATION NUMBER: PCT/JP00/00490
; PRIOR FILING DATE: 1999-01-28
; PRIOR APPLICATION NUMBER: JP 11-205229
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: JP 11-22427
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 506
; TYPE: PRT
; ORGANISM: *Perilla frutescens*
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of a protein having an activity too
; OTHER INFORMATION: directly convert flavanone to flavone
US-09-672-785-8
Query Match 38.6%; Score 921.5; DB 2; Length 506;
Best Local Similarity 38.9%; Pred. No. 1.6e-106;
Matches 190; Conservative 91; Mismatches 183; Indels 25; Gaps

```

QY 93 LQXKXETXKTEPQTSAXRXLTVDXVXXXPXGPMXFEVRLLIMNDLXNATVXXLRPLR 152
Db 85 LKTHIELV-FSSRKHSTALDIYVDBSFPASPYGGMKFIKLCCTYELLGARNLAHQPIR 143
QY 153 TQOIRKRLXMXAQAEMAKPDLXTEELIKMXNSTXSMXL-----GEAEIRDIARE 204
Db 144 TLEVKSFLOILMRKESGSEFVNVETELKLTNSNI SHMULSIRSETESEEAARYIRE 203
QY 205 VUKIXGSEVLTPFIKPLKLVGXEKVIDDLINKFPDVEVRVIKKRXIIVRRXNEXX 264
Db 204 VTQIFSEFVSDIIMLCNKPDPQGRKGSBDIQRYDALLEKITDBEK--QRTHGGG 261
QY 265 EGEKSGVXLDTLLEPADETXEIKTKXXIXGLVVDKFSAGXSTAXXTMALAELINP 324
Db 262 GGGEADPFLDMFELDIMESGKAEMKFTREHLXALILDFPTAGTDPTTALVCEMALAEVINP 321
QY 325 XVLXXAREXSVYGKDXLVDEDPQNLPTYRAIVKETFFRHPPLPVVKRCKEEXING 384
Db 322 NVLKKAQBEIANVGDRILOESDAPNLPYQALKEIFRHPPIPMILARKSISDCYIDG 381
QY 385 XVXPEGALXFNVMQVGDXTWDRPSEKRPBRLFETXABEAXXLDLRGHPOLLPGS 444
Db 382 YMIIPATLILFVNIMSGRNPKIMDPYTAFOBERPLEK---EKAATVKGQHFEELFPGT 437
QY 445 GRMXCGVXLATSGXATLLASLIOGFDLOVLGPOQOILKGXDATVSMEEBAGLVPFPAHS 504
Db 438 GRGCGCFMILAIQDEVIIITGMIIQCFDWKL--PDG-----SGHYMDABERGLTAPRETD 489
QY 505 LVCPVLARI 513
Db 490 LFCRVVPRV 498

```

```

RESULT 5
US-09-351-229-4
; Sequence 4, Application US/09351229
; Patent No. 6380465
; GENERAL INFORMATION:
; APPLICANT: Barrett, Michael
; TITLE OF INVENTION: Cytochrome P450 Enzymes and Related Compounds and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: P-1049
; CURRENT APPLICATION NUMBER: US/09/351,229
; CURRENT FILING DATE: 1999-07-11
; EARLIER APPLICATION NUMBER: 60/092,596
; EARLIER FILING DATE: 1998-07-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Zea mays
US-09-351-229-4

Query Match      27.2%; Score 651; DB 2; Length 513;
Best Local Similarity 32.6%; Pred. No. 1,6e-72;
Matches 164; Conservative 89; Mismatches 200; Indels 50; Gaps 13.

```

Oy 33 PNPSPXRRLPFIGHKLKDKLHYAXIDSKKHGLFSXXGSPVTVAISPELFKFL 92
| | | | | : | | | | | : : : | |
Db 27 PYPPQPP-LPIGLHLIGPR-IHQTPHDLSQRYGLMQLRIGSRICVIAASPELAACC 84

QY 35 PPSPKRLPLFGCHKLLMDKLLHYXKIDLSKGGHGFSXSFSSMTLVASTLEFLFQ 94
 Db 29 PGPPP-WTIGNLNM-GELPHRSNNELSKRYGFLMQLMFSSLEPVVVGASAMAKLFLK 86
 QY 95 XXEATSFYRFQTSAXRLTYD-XXVAXXKXPYXFWKLIMNDLXNATVNXKLPLFT 153
 Db 87 TMDA-AFSDRPRPAVGKTYADDCSGLMAFPFPYLROARRICATELFSATRLSEFEHID 145
 QY 154 QQIRKKLRMAQXAEKKRLDTTEELTKKXNXTSMMLGE----- 194
 Db 146 EERKWLRLQRAAGTYRLRDYQML-ALGVISRTVIGKYYWEEAADGEGDSNPAT 203
 QY 195 AEIRIDIAEVLKIXGYESLTDFIXPKLKLKYGTEKRIIDLLINKEDPYVERYL--KRR 251
 Db 204 PAFEFREMDVFPALGAFNIGYITFPLDMLDQGVAAKKKKKARGRLERLDVHNER 263

```

QY      RXIVRRRXNEXXEGXSGXYLDTLLEFDEDETEIKTKKXIXGLVVDXFSAGDSTAX 3111
D6      RL-----REGGNFAKD-----MDVLILQTLADDTSLSEVLQSRONVKAITODDLIACTSDNAN 3115
QY      XTWMALAEILINNPXYLXXAREEYXSVGKDXLVDEVDTONLPYIRAIYKETFRRNHPPLV 3711
D6      TLFWASSELKNKRIILAKAMEELNHYIRDRILVTESDLPRIPLYEALVKEIMRNVHPAPM 3757
QY      V-RRKCKEEXCINGXYXPGALXKXPFVMOVGDXKYMPDPESEPERELETXAEGEAXXL 4305
D6      LAPHVAREPDSVDGYVLAGTVLFINVMAIIGDPCGMADPEEFRREREVES-----KI 4328
QY      DLRGXHFOLLPESGEXMCPGVXYLATSGXYATLTLASLIQCPLDQVLGPGOQLIKGDAKVS 4905
D6      DVGHHGFOLLPFSGSGRMCPGIIMLAKVMALSIANLHGFEMRL--PGVTAAE-----ELS 4982
QY      MEERAGLTVPRASHIVCPVLARI 513
D6      MDEAFKLAIVRKFFLWVVAEPRL 505

```

```

RESULT 6
US-09-142-108C-17
; Sequence 17, Application US/09142108C
; Patent No. 6774285
; GENERAL INFORMATION:
; APPLICANT: Brugniera, Filippa
; APPLICANT: Holtom, Timothy A.
; APPLICANT: Michael, Michael Z.
; TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOID PATHWAY ENZYMES
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: 11658
; CURRENT APPLICATION NUMBER: US/09/142,108C
; CURRENT FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: PN8386
; PRIOR FILING DATE: 1996-03-01
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Chrysanthemum
US-09-142-108C-17

```

| | | | | |
|-----------------------|-------------------|--------------------|------------|-------------|
| Query Match | 26.7% | Score 637.5; | DB 2; | Length 508; |
| Best Local Similarity | 30.7% | Pred. No. 7.7e-71; | | |
| Matches 162; | Conservative 101; | Mismatches 208; | Indels 57; | Gaps 14 |

| | | | |
|----|-----|---|-----|
| Oy | 5 | LAAGLXVLAFFXHLRPRPXKXSKALNHLNPPSPXP-RLPFIIGHXHLKMDKILNYXHI | 61 |
| Db | 11 | LIIG-SVLVFLNL-----SSRKXARLRPPGPTWIVGNLHLG-----PIPHNALA | 56 |
| Oy | 62 | DLKKGGRFLSXFFGSMPTVASTPBEFLKFLPLOXHAITSFXTRPQTSAXKXKILYD-XXVA | 120 |
| Db | 57 | ALAKKQYPLMHLRLRGCDVVVAASASVAQFLKMHDA-NFASRPNPSGAKVVAANYODLV | 115 |
| Oy | 121 | XXRXPWXXFVVRKLIIMDLNKNATTVXKLRPLRTOQIRKCLRMAOXAEKXKRLDXTBEYL | 180 |
| Db | 116 | FAPYGPFRMLRLRKICSVHLFSAKALDPFHVRGEVAVLTVLLSAGNS--PVQIGQOLN | 173 |
| Oy | 181 | KKXNXYSSMMKLG-----EABEIRDLAEVLKIXGESLUDFLYPLKALKVGYKE | 230 |
| Db | 174 | VCATNALARWLGRVFGDGDIDRSNAEFKDMVVELVNLAGEPNLDGFLVULDFLQGIT | 233 |
| Oy | 231 | KRIDDLINKEDPVVERIVKIKRRIYBRNKNXGEXXEGXSGVKILDTLFEAEDEYE-IKI | 285 |
| Db | 234 | KKKMKLHYRPFSLKIVENHT-----APGLGHTDLLSTLISLKODADIEGKL | 286 |
| Oy | 290 | TKXXIXGLVVDXPSAGKDSIAKXTWALAEILNNPVLXXABEEXSVYGKDLVDEYDT | 344 |
| Db | 285 | TDWEIKALLNLNFAAGTDTSSSTVEAMIAELLRNHPOILQOABEEEDIAVVGQDRLTETDL | 344 |

```

QY      350 QNLRYRALVKEPRRHHRLPV-VRRKXEEEXINGXVREGALXXFNWVOVGDXKCYD 408
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      345 SOLTYQALVKEPRRHHRLSPRLISESECVGGYITRGSTLLNVMAIADPPGMA 404
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      409 RPEXRPERFLETXAGEAXXLDRGKHFOILLPGSGRGMCPGYXLATSGATLTLASLIQ 468
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      405 DPLEFPFRFL---PGEGKPADVAGNDFVYIPGAGRRICAGMSLGRMWQLLIATLVQ 461
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      469 CPDLQV---LGPQGLIKGDXAKVMEERAGLTVPRASLSLVCVPLARI 513
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      462 TTFWELANGLERP-----MLNMEAYGTLTORAPLNVHKKPRL 500
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

RESULT 7
US-09-689-783A-2
; Sequence 2, Application US/09689783A
; Patent No. 6605469
; GENERAL INFORMATION:
; APPLICANT: KANG, JEONG-GU
; APPLICANT: PARK, CHUNG-MO
; TITLE OF INVENTION: NUCLEIC ACID MOLECULE ENCODING A CYTOCHROME P450 HYDROXYLASE IN
; TITLE OF INVENTION: BRASSINOSTEROID BIOSYNTHESIS IN PLANTS
; FILE REFERENCE: 107572
; CURRENT APPLICATION NUMBER: US/09/689,783A
; CURRENT FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Pisum sativum
US-09-689-783A-2

```

```

Query Match 156: 26.3%; Score 629; DB 2; Length 495;
Best Local Similarity 31.8%; Pred. No. 8, 7e-70;
Matches 156; Conservative 85; Mismatches 192; Indels 58; Gaps 13;

QY 35 PPSPPRLPEFGHMLKDKLHYAXNIDSKGHPLFSXXGSMPTVASTPELFKFLQ 94
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 36 PGPGRP-WPIIGNFNLI-CTLPHQSLHGLTKGPIIMHLMFGSKRVVGSSTVEAKAFPK 93
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 95 XKEATSEKTRFOTSAXRKLTYP-XAVAXXPKQGYMKFVRLINMDLNATTVMKRLRT 153
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 94 THDAT-LAGRPFSAGKTYTYNSDITWSQYGYWRQARRMCLLEFSARLESYEYTRK 152
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 154 QOIRKXLRMAQXAEAXKPELDYTEELLKMXNSTXSMXKLG-----EAEETRDI 201
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 153 QELHAFLEHLEPFSRN--KTIILKDHLSSLSLANSVISMVLRKYLEKVENSIISDFEKRM 210
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 202 AREVLKIXGEYSALTDFIXPLKXLYKGYEKERRIDILINKEDPVVERVIKKRRXIVRRXNG 261
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 211 LDLEFLNLGIIINIGDIPIMHFLDFQGYKRMKVLSKKFDGFMENHVEEH--IERRK-- 265
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 262 EXXEGEXSV-----XUDTLLEPAEDTEXIKITKXXIXGLVNDXFSGXOSTAXXTE 314
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 266 -----GVKDYVAKDMVDVLLQLAEDDPLEYKLERRHGKAFATODILAGTSBSAATVE 317
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 315 WALAEILNPPYVLXXAREEXYSVVGKDXLYDEVDTONLPIYIRAIKETPFMAHPPLP-VVK 373
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 318 WAISELIRPELEFKQATELDRVIGRERWEEEDIANLPVYVAIAETMMLHPAPMILVP 377
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 374 RKCEBXGXNGXVPEGALXXFNVWQVGDXXKYWDPSSEKRPERFLETXAEGEAXXLDLR 433
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 378 RAREEDCNINGDIPKGSLLIVNTWTIARDSNVNDNNEPMPERFL-----GKDIDVK 430
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 434 GXHFQLLPFGSGRXMCPGYXLATSGAATLASLIQCFDLOVLGPQGIILKGDAK---VS 490
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 431 GHDYELLPPGAGRMRMCPGYPLGIKVIQSSILANLHGFNWL-----SDVKKEDLN 481
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 491 MEERAGLTVP 501
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 482 MEIRFGLSTPK 492
   |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

```

RESULT 8

US-09-142-108C-6

Sequence 6, Application US/09142108C

Patent No. 6774285

GENERAL INFORMATION:

APPLICANT: Bruggiera, Filipa

APPLICANT: Bruggiera, Timothy A.

APPLICANT: Michael, Michael Z.

TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOID PATHWAY ENZYMES

TITLE OF INVENTION: AND USES THEREFOR

FILE REFERENCE: 11658

CURRENT APPLICATION NUMBER: US/09/142,108C

PRIOR FILING DATE: 1998-09-01

PRIOR APPLICATION NUMBER: P8386

NUMBER OF SEQ ID NOS: 45

SOFTWARE: Patent In Ver. 2.1

SEQ ID NO 6

LENGTH: 512

TYPE: PRT

ORGANISM: Antirrhinum majus

US-09-142-108C-6

Query Match 26.2%; Score 626; DB 2; Length 512;

Best Local Similarity 30.3%; Pred. No. 2,2e-69;

Matches 162; Conservative 94; Mismatches 216; Indels 62; Gaps 14;

1 MLLELALGLXVLALEFXHRLPTXANXSKALRLPNPSPXP---RLPFGHKLHLDKLIH 57
 19 LVPCTFLIGLFLVLSFL-----NKKVKPLPPGKFWPVGNIPLHGLPKP-----H 64
 58 YAXIDLSKGGGLFSXFGSMPTVVASTBELFKLFOXXEATSEKTRPQTSAXXLYTD- 116
 65 QSMALARVHGPILHLKGFVHVVAASASVAEKFKVDA-NFSRPPNSGAKHVAHY 123
 117 XXVAXXPGPYXKFXVKLIMNDLXNATVNLRLPTQOIRKQLXMAQXAEAXXPLDXT 176
 124 QDLVPAFYGPFRMRMLRKICALHLFSKALANDPTNRQDEVLITRLADAGET--PLKLG 181
 177 BELLKWXSSTXSMMLG-----EAEIRDIAREVLKIXGEVSLDTFYLKXL--- 224
 182 QMMNTCATNAIARVMLGRVVGHADSKAEFEKAMVVELVLAGVFMIGDFIPLLEKLDIQ 241
 225 ----KVGKTEKRIIDLINKEFDPVEVEVITKRRKIVARRXNGEXXEGXSGVXLDTLLEPA 280
 242 GVIARKKKQLHRLPDSFLK-----ILGDHKINSSDEYKGSDDLMLMLISLK 287
 281 E-DETXEIKITKXXIXGLVVDXPSAGXSTAXXTETWALAEILNPNXYLXXAREEXYSVVG 339
 288 DADDAEGGRITDVEIKALLNLNFAAGTDTTSTVEICIAELVHNPILAQVQKELDSVVG 347
 340 KDXLVDEVDTQNLPIYRAIVKETFRMHPPLV-VKCKXCECKXINGVXVPEGALXXFNW 398
 348 KRRVVEADLAGLPFLQAVVKEVFRILPSTPLPRIAHSCVENVYLLIPKSTLLLVNW 407
 399 QVQXDKKXVDRPSEKPERPLETAXAGEAXXLDLKGXHPQLPFGSGRMCPGVXLATSG 458
 408 ALARDNVVDEPLEPFRFLK--GSEKPNVDVNRGNDLELFPFGGRICAGMSIGIRM 464
 459 XATLLASLIQCFDLQVIGPQGIILKGDAXVSEEBRAGLTVPRASHLVCVPLAR 512
 465 VQLTITLINAFFPDL--ADGQL-----PESLNNEBAVGLTQADAPLVVHPKR 512

RESULT 9

US-09-142-108C-15

Sequence 15, Application US/09142108C

Patent No. 6774285

GENERAL INFORMATION:

APPLICANT: Bruggiera, Filipa

APPLICANT: Bruggiera, Timothy A.

APPLICANT: Michael, Michael Z.

TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOID PATHWAY ENZYMES

TITLE OF INVENTION: AND USES THEREFOR

FILE REFERENCE: 11658

CURRENT APPLICATION NUMBER: US/09/142,108C

PRIOR FILING DATE: 1998-09-01

PRIOR APPLICATION NUMBER: P8386

NUMBER OF SEQ ID NOS: 45

SOFTWARE: Patent In Ver. 2.1

SEQ ID NO 15

LENGTH: 513

TYPE: PRT

ORGANISM: Rosa hybrida

US-09-142-108C-15

Query Match 26.1%; Score 623; DB 2; Length 513;

Best Local Similarity 31.4%; Pred. No. 5,2e-69;

Matches 161; Conservative 89; Mismatches 205; Indels 58; Gaps 16;

27 KALRH-LENPSPXPRLPFGHX-HLKDKLIYAXIDLSKGGPLFSXFGSMPTVVA 84
 23 KSRHSILPLPGPKP-WPVGNLPHL--GPRHHSIALAKKGLPLMLRLGVYDVVVA 79
 85 TPFLFKLFOXXEATSEKTRPQTSAXXLYTD-XXVAXXPGPYXKFXVKLIMNDLXNAT 143
 80 SASVAQGLKTHDA-NFSRPPNSGAKHLAVNYODLFRPGPRMRFRKISSVHLBSGK 138
 144 TVNKLRLPTQOIRKQLXMAQXAEAKKPLDXTTELLKWNXSTXSMMLG----- 193
 139 ALDILKVRQGEVSLMALAN--SGSKVYLAQNLNCTNALGRVWGRVFGDSGG 196
 194 --EAEIRDIAREVLKIXGEVSLDTFYLKXL-----KVGKTEKRIIDLINKEFDPV 243
 197 DDPKADERSKVMVEMVLAGVFNIGDFIPSLBWLIDQVASKMKKLHGRFDFLT----- 251
 244 VERVYKRRKIVRRKXNEXXEGXSGVXLDTLLEFADEXE-IKIKXXIXGLVVDX 302
 252 -----AIVEDHKGSSTAGVHD--MLTTLTSLKEDADGEGKLTDTBKALLNMF 300
 303 SAGXSTAXXTETWALAEILNPNXYLXXAREEXYSVVGKDXLVDEVDTQNLPIYRAIVET 362
 301 TAGDTSSSTYEMAIABELIRHPHMLARQKELDDPVGHDRLVTESDINLPYLAQVRET 360
 363 FRMHPPLV-VKCKXCECKXINGVXVPEGALXXFNWQVGDXXKXVDRPSEKPERPLET 421
 361 FRLHSTPLSLPRMAESCEINGYHIPKSTLLVWVAISRDPAMADPLEKPERFL-- 418
 422 XAEAXXLDLKGXHPOLLPGSGXMGCPGVXLATSGAATLLASLIQCFDLQVLPQGI 481
 419 -PGGEKPNVDIRGNDPEVIFPGAGRICAGMSGLRMVHMLTATLVHAFN-----WAL 470
 482 LKGDAX-KVSEBRAGLTVPRASHLVCVPLARI 513
 471 ADGLTAEBKLNDEAVGLTQRAAPLWHPRRRL 503

RESULT 10

US-09-292-768-2

Sequence 2, Application US/09292768

Patent No. 6134185

GENERAL INFORMATION:

APPLICANT: Croteau, Rodney B

APPLICANT: Lupien, Shari L

APPLICANT: Karp, Frank

TITLE OF INVENTION: LIMONENE HYDROXYLASES

TITLE OF INVENTION: RECOMBINANT MATERIALS AND METHODS FOR THE PRODUCTION OF

FILE REFERENCE: wslu13463

CURRENT APPLICATION NUMBER: US/09/292,768

PRIOR FILING DATE: 1999-04-14

PRIOR APPLICATION NUMBER: 08/881,784

EARLIER FILING DATE: 1997-06-24

NUMBER OF SEQ ID NOS: 70

SOFTWARE: Patent In Ver. 2.0

```

; SEQ ID NO 2
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Mentha spicata
US-09-292-768-2

```

| | | | | |
|-----------------------|------------------|--------------------|------------|-------------|
| Query Match | 25.9%; | Score 618.5; | DB 2; | Length 496; |
| Best Local Similarity | 29.6%; | Pred. No. 1.8e-68; | | |
| Matches 146; | Conservative 93; | Mismatches 214; | Indels 41; | Gaps 14 |

| | | | |
|----|-----|---|-----|
| QY | 26 | SKALHLENNPBPXPRLPTIGXNHLKDKLILNAXLDLSKDDPLESSXXGSPMTVAJST | 85 |
| Db | 28 | SKSQGNL--PBP-PKLPVIGLHFLIMGSLPQCVFVSINQKYCPVAHVQDGEVYSLVS | 84 |
| QY | 86 | PELFLFLQXHXATSEFXTRPQTSAXKXLYTD-XXVAXXKXPYWXFVKRLIMNDLXNATT | 144 |
| Db | 85 | AEEAQAQAKVLVD-PNFADRFDDIGSRTMWYDKDDILFSPYNDHMQRRLCVTELLSPKN | 143 |
| QY | 145 | VNXLRLPRLTQIRKKLRXMAQXAEAKPLDXTBEILLKMNSTXSMXGLG---EAEIIRD | 200 |
| Db | 144 | VRSFGYIIOEBTELRLRLIGSSGGA--PDVYTBVEVKMCCVVCRAFGSLVKDQGSIAE | 201 |
| QY | 201 | IAREVLKTXGEYSLTDFIYP---LKQLKVGKYEKRIIDILINKFDPVEYRVIKKRXIYR | 256 |
| Db | 202 | LYKESLIALASGELELD-LYPSMWLNLILSLINKY-RLQMRRLRDLHILGFELEHR--- | 254 |
| QY | 257 | RRXNGEXXEGEXSGVXL-DTLEPFADETXEIKITKXXIXGLVNDPFSAGXDSTAXTWM | 315 |
| Db | 255 | -----EKSGBEGGEDYVDVLFPMQKGSIDKIPITSNCTKGFJDFPFSACAEISSTTISW | 309 |
| QY | 316 | ALABELINNPXYLXXHAREEXYSVVGKXJLVDEVDTOMLPYIRALIVKTEFRMNPRLPVVKRK | 375 |
| Db | 310 | ALSEILMRPDAKMAKQAEVREALKKGTIVVDLSVEQLEKTLRSVLKETLRLHRPPRLIPRQ | 369 |
| QY | 376 | CXEBKXNGXVYRBEGLAXXFNWQVQXDKKYMDRBEXKPERRLTXHABEAXXLDLRGX | 435 |
| Db | 370 | SREBEVNGYTIIPAKTRIFINWALIGRDQOYMEDPRTGERPERDEVSR-----DFMGN | 422 |
| QY | 436 | HFQLLPFPSSGRMCEGVXLATSGXATLILSLIQCPLOVLGPPGQILIKGXDAKVSNEERA | 495 |
| Db | 423 | DFEFLPFGAGRRICGILHFGLANVELPRLAQDLNHPMKL--PQGM-----TDADLDITETP | 476 |
| QY | 496 | GLTVYRAHSLVCP 509 | |
| Db | 477 | GLSGEKKXNVCLVP 490 | |

```

RESULT 11
US-09-292-768-66
; Sequence 66, Application US/09292768
; Patent No. 6194185
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney B
; APPLICANT: Lupien, Shari L
; APPLICANT: Karp, Frank
; TITLE OF INVENTION: RECOMBINANT MATERIALS AND METHODS FOR THE PRODUCTION OF
; TITLE OF INVENTION: LIMONENE HYDROXYLASES
; FILE REFERENCE: wsaui3463
; CURRENT APPLICATION NUMBER: US/09/292,768
; CURRENT FILING DATE: 1999-04-14
; EARLIER APPLICATION NUMBER: 08/881,784
; EARLIER FILING DATE: 1997-06-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Artificial Sequence
; US-09-292-768-66

```

| | | | | |
|-----------------------|------------------|--------------------|------------|-------------|
| Query Match | 25.9% | Score 618.5; | DB 2; | Length 496; |
| Best Local Similarity | 29.6% | Pred. No. 1.8e-68; | | |
| Matches 146; | Conservative 93; | Mismatches 214; | Indels 41; | Gaps 14 |

```

OY 26 KKAJLHNPSPSPXRPLPEIFGHXHLXOKLHAYAXIDSKKHGPLESSXXFGSPMPVAST 85
Db 28 SKQOQNL--PSP-PKLPYIGHLHLMGGLPOHVRSTIOKQIGVAHVOLGEVYSVLSS 84
OY 86 PELFLFLQXXEATSFXTRFQTSAXRXLYTD--XXVAXXPXGYPXKVRKLIMNDLXNATT 144
Db 85 AEAQAQKAKVLD--PWFADRFPGDIGSRTWYDDEIIFSPYNDHMROMRICTVELLSPKN 143
OY 145 VNXLRPLFTQOIRKCLRMAQXAEAXKPLDTEELLKMXNSUXSMWXLG----EABEIRD 200
Db 144 VRSFGYIIOEBELERLIRLIGSSGGA--PFDVTEEBYSKNSCVVVCRAFSGLKQOSLAE 201
OY 201 IAREVLKIXGEYSLTDFTXP----DKXLKVGYEKRIDDLINKFDEVERVIKRRXYLR 256
Db 202 LVKESLIALASGPELAD--LYPSSWMLNLTSLNXY--RLQSMRRRLDHIILGFLSEHR---- 254
OY 257 RRXNEXXEGESGXUL--DTLLEFADETXELKITKXXIXGI-VNXXFSAGXSTAXXTW 315
Db 255 ----EKSGEGEGGDIVDLVFRMOKSGDIKPIITSNCIKGIFPDFSAGAESSTTISW 309
OY 316 ALAELINNPXYLXAXAREEXYSVVGKDXLVDDEVDTQNLPHYRAIRIVKETFMHPRLPVVKRK 375
Db 310 ALSELMRNPAPKAKAQAEVREALKCKTUVLDSEVOELKTRSVLXETTLRLHPFPLIPRO 369
OY 376 CXEEXXINGXYAPBEALXXFNWQGXKXKWDPRSEXPPEPFLFXAGEXAXXLDRX 435
Db 370 SREBEVNGYIIPAKTRIFINWALGRDQYVEDPDRFBEPFDEVS-----DFMGN 422
OY 436 HFQQLPFSGGRMCPGVNLATSGXATLLASLIQCPDLQVLAGOGQOLIKGXDAKVSMEERA 495
Db 423 DPEFPFGAGRRIICGHLHGLANVEIPLAQOLLVHFDMKL--PQGM----TDADLDWTERE 476
OY 496 GLTVPRASLSVCP 509
Db 477 GLSGRPKKNVCLVP 490

```

```

1      RESULT 12
2      US-08-881-784-1
3      , Sequence 1, Application US/08881784
4      , Patent No. 6083731
5      , GENERAL INFORMATION:
6      , APPLICANT: Croteau, Rodney B.
7      , APPLICANT: Lupien, Shari L.
8      , APPLICANT: Karp, Frank
9      , TITLE OF INVENTION: RECOMBINANT MATERIALS AND METHODS FOR
10     , TITLE OF INVENTION: THE PRODUCTION OF LIMONENE HYDROXYLASES
11     , NUMBER OF SEQUENCES: 58
12     , CORRESPONDENCE ADDRESS:
13     , ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
14     , ADDRESSEE: PL/C
15     , STREET: 1420 Fifth Avenue, Suite 2800
16     , CITY: Seattle
17     , STATE: WA
18     , COUNTRY: USA
19     , ZIP: 98101
20     , COMPUTER READABLE FORM:
21     , MEDIUM TYPE: Floppy disk
22     , COMPUTER: IBM PC compatible
23     , OPERATING SYSTEM: PC-DOS/MS-DOS
24     , SOFTWARE: PatentIn Release #1.0, Version #1.30
25     , CURRENT APPLICATION DATA:
26     , APPLICATION NUMBER: US/08/881,784
27     , FILING DATE:
28     , CLASSIFICATION: 435
29     , ATTORNEY/AGENT INFORMATION:
30     , NAME: Shelton, Dennis K.
31     , REGISTRATION NUMBER: 26,997
32     , REFERENCE/DOCKET NUMBER: WSUR19777
33     , TELECOMMUNICATION INFORMATION:
34     , TELEPHONE: (206) 224-0718
35     , TELEFAX: (206) 224-0779

```



```

1      INFORMATION FOR SEQ ID NO: 1:
2      SEQUENCE CHARACTERISTICS:
3          LENGTH: 496 amino acids
4          TYPE: amino acid
5          STRANDEDNESS:
6          TOPOLOGY: linear
7      MOLECULE TYPE: protein
8      ORIGINAL SOURCE:
9          ORGANISM: Mentha spicata
10         IMMEDIATE SOURCE:
11         CLONE: SM12.2
12     FEATURE:
13         NAME/KEY: Cleavage-site
14         LOCATION: 7..27
15     OTHER INFORMATION: /note= "V-8.2 proteolytic fragment"
16     FEATURE:
17         NAME/KEY: Active-site
18         LOCATION: 7..48
19     OTHER INFORMATION: /note= "Membrane insertion
20     OTHER INFORMATION: sequence"
21     FEATURE:
22         NAME/KEY: Active-site
23         LOCATION: 44..48
24     OTHER INFORMATION: /note= "Halt-transfer signal"
25     FEATURE:
26         NAME/KEY: Cleavage-site
27         LOCATION: 182..206
28     OTHER INFORMATION: /note= "V-8.1 proteolytic fragment"
29     FEATURE:
30         NAME/KEY: Cleavage-site
31         LOCATION: 380..404
32     OTHER INFORMATION: /note= "V-8.3 proteolytic fragment"
33     FEATURE:
34         NAME/KEY: Binding-site
35         LOCATION: 429..454
36     OTHER INFORMATION: /note= "Heme binding region"
37     US-08-881-784-1

```

OY 496 GLTVPRAHSLVCVP 509
 || : || : ||
 Db 477 GLSGPKKKKNCVLP 490

RESULT 13
 US-09-292-768-4
 ; Sequence 4, Application US/09292768
 ; Patent No. 6194185
 ; GENERAL INFORMATION:
 ; APPLICANT: Croteau, Rodney B
 ; APPLICANT: Lupien, Shari L
 ; APPLICANT: Karp, Frank
 ; TITLE OF INVENTION: RECOMBINANT MATERIALS AND METHODS FOR THE PRODUCTION OF
 ; TITLE OF INVENTION: LIMONENE HYDROXYLASES
 ; FILE REFERENCE: waur13463
 ; CURRENT APPLICATION NUMBER: US/09/292,768
 ; CURRENT FILING DATE: 1999-04-14
 ; EARLIER APPLICATION NUMBER: 08/881,784
 ; EARLIER FILING DATE: 1997-06-24
 ; NUMBER OF SEQ ID NOS: 70
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 4
 ; LENGTH: 500
 ; TYPE: PRT
 ; ORGANISM: Mentha piperita
 ; US-09-292-768-4

DQ 436 HFQLLPFGSGRRMPCGYXLANSGXATLTASLIQCFLDQVLGPRQGQLIKGRDAKVSMEERA 495
 : : : : :
 DB 423 DEEFIFPGAGRIICPGLHFGLNVEIPLAQLLHYFDWKL--PQGM---TDADLLMTETP 476

RESULT 14
US-09-292-768-68
; Sequence 68, Application US/09292768

```
/ Patent No. 6194185
/ GENERAL INFORMATION:
/ APPLICANT: Croteau, Rodney B
/ APPLICANT: Lupien, Shari L
/ APPLICANT: Karp, Frank
/ TITLE OF INVENTION: RECOMBINANT MATERIALS AND METHODS FOR THE PRODUCTION OF
/ TITLE OF INVENTION: LIMONENE HYDROXYLASES
/ FILE REFERENCE: wau13463
/ CURRENT APPLICATION NUMBER: US/09/292,768
/ CURRENT FILING DATE: 1999-04-14
/ EARLIER APPLICATION NUMBER: 08/881,784
/ EARLIER FILING DATE: 1997-06-24
/ NUMBER OF SEQ ID NOS: 70
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 68
/ LENGTH: 500
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
US-09-292-768-68
```

```
Query Match      25.8%; Score 616.5; DB 2; Length 500;
Best Local Similarity 29.6%; Pred. No. 3.3e-68;
Matches 145; Conservative 91; Mismatches 207; Indels 47; Gaps 11;
```

```
QY 35 PPSXPRLPFIQXHLKDKLHVAXIDSKKHGFLFSXXFGSMPTVASTPELFLKFLQ 94
DB 36 PPGP-PKLPILGHLHLWGLPQHALLASVAKQGPVAVHQLGEVFSVLSREATKAMK 94
QY 95 XKEATSPKTRPQTSAXRKLTYD-XXVAXXPXGPYXKLVKLMNDLXNATTYVXLRPLRT 153
DB 95 LVD-PACADRFESIGTKIMWYDNDITFSPYSVHWQMKRICVSELSARNVRSFGFIKQ 153
QY 154 QOIRKILKXMAOXAAXKPLDYTEELLKXNSTXSMMXLG---EAEIRIDIAREVLIKX 209
DB 154 DEVSLHLGHLRSSAAAGEAVDLTERIATITCSIIICRAAGSVIRHDEHVELVKALMSA 213
QY 210 GEYSITDFIXPKL-----KVGKYEKRIDILINKPDEVVERVIKRRXIVERRXNG 261
DB 214 SGFELADMPSSSKLNLICWNKSKLWRMRARVDALIEAI--VEBHKLK----- 260
QY 262 EXKBEXGV-XLDTLLEFADETXEIKTKXXIXGLVVDXFSAGDSTAXXTWALAE 320
DB 261 ---SEFGEEDIIIVLFEMQKDSQIKVPIITTAIKAFIDTFSAGETISSTTLVWMAEL 317
QY 321 INNPVYLXAXAREEXYSVVGKDLVDEVDTQNLPIYIRAIYKETFMRMHPPLVVKRCXEBEC 380
DB 318 MRNPEVMAKQAQAEVAAALAGKTDMDVDVQELKYMKSVMKTRMRHPIPLPRSCREEC 377
QY 381 XINGVXPEGALXXFNWQVGDXXKYMWRPSEKRPREFLETYAEGEAXXLDLGGXHPOLL 440
DB 378 EVNGYTIPIKARIMINVMGMRNPPLYWEKETFWPERF-----DQVSRDFMGDFBFI 430
QY 441 PPGSGRXMCPGVXALTSGLATLASLIQCFDIQVLGPOQIILKGD-AVNSHEBBAGLTV 499
DB 431 PFGAGRRIICPGLNFGLANVEPLAQLLYHF-----WKLAEGMNPDSMDSEAGLGTG 483
QY 500 PRAHSLVCP 509
DB 484 IRKNMLLVF 493
```

```
RESULT 15
US-09-142-108C-2
/ Sequence 2, Application US/09142108C
/ Patent No. 6774285
/ GENERAL INFORMATION:
```

```
/ APPLICANT: Bruguiera, Filippa
/ APPLICANT: Holton, Timothy A.
/ APPLICANT: Michael, Michael Z.
/ TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOID PATHWAY ENZYMES
/ FILE REFERENCE: 11658
/ CURRENT APPLICATION NUMBER: US/09/142,108C
```

```
/ CURRENT FILING DATE: 1998-09-01
/ PRIOR APPLICATION NUMBER: PN8386
/ PRIOR FILING DATE: 1996-03-01
/ NUMBER OF SEQ ID NOS: 45
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2
/ LENGTH: 512
/ TYPE: PRT
/ ORGANISM: Petunia x hybrida
US-09-142-108C-2
```

```
Query Match      25.8%; Score 616.5; DB 2; Length 512;
Best Local Similarity 30.7%; Pred. No. 3.4e-68;
Matches 153; Conservative 96; Mismatches 209; Indels 41; Gaps 13;
```

```
QY 32 LPNPSXPRLPFIQXHLKDKLHVAXIDSKKHGFLFSXXFGSMPTVASTPELFLK 91
DB 31 LPLPPGP-PKLPILGHLHLWGLPQHALLASVAKQGPVAVHQLGEVFSVLSREATKAMK 88
QY 92 FLOXXEATSPKTRPQTSAXRKLTYD-XXVAXXPXGPYXKLVKLMNDLXNATTYVXLRPLRT 150
DB 89 FLKTHDA-NFSSRPNSGAEHMAVYQDLVFPAPGPRWRMLRKICSVHLFSTKALDDPRH 147
QY 151 LRTQOIRKILKXMAOXAAXKPLDYTEELLKXNSTXSMMXLG---EAEIRIDIAREVLIKX 197
DB 148 VRODEVKTLTTRALASAGQ--KPVKLGLLVCTTNALARVWLGRKVFADSGSDVDPPQAAE 205
QY 198 IRDIAREVLKIXGEYSITDFIXPKLKVGYEKERIDILINKPDEVVERVIKRRXIVRR 257
DB 206 FKSVMYEMMVAVAGVFNIDFIPLQNLMDIQGVAAKMKLHARFADFLLDIEBHNG----- 261
QY 258 RXNGEXXEGEXSGVYLDLLEFADETXEIKTKXXIXGLVVDXFSAGDSTAXXTW 315
DB 262 KIFGEMKQ-----LSTLISLKDNDADNDGKLTDEIKALLNLVFAAGTDTSSSTVEW 315
QY 316 ALAEILNPPVYLXAXAREEXYSVVGKDLVDEVDTQNLPIYIRAIYKETFMRMHPPLV-VKR 374
DB 316 AIAELIRNPKLIAQAOQEDIDRVVGRDLVGBELDIAQLTYLEAIYKETFRLHPSPLSPR 375
QY 375 KCXEXCXINGVXPEGALXXFNWQVGDXXKYMWRPSEKRPREFLETYAEGEAXXLDLGGXHPOLL 434
DB 376 IASECEINGNFIPIKGSITLLNVMARIADPNAMADPLEFRERFL---PGGEKRVNDVRG 432
QY 435 XHFOLLPPSGRXMCPGVXALTSGLATLASLIQCFDIQVLGPOQIILKGDADAKVSMER 494
DB 433 NDFEYIIPGAGRRIICAGNMLGIRWQMIATLIIHFNMDLV--SGQL-----PEMLMMEA 486
QY 495 AGLTVPRAHSLVCP 513
DB 487 YGLTIQRADPLVHPRPL 505
```

```
Search completed: December 22, 2005, 00:04:00
Job time : 47 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: December 22, 2005, 00:04:04 ; Search time 260 Seconds

(without alignments)
3561.960 Million cell updates/sec

Title: US-09-857-581b-66

Perfect score: 2389
Sequence: 1 MLELALGXVLAFLXHLRP.....ASHLVCVPARIGVSKLAS 521

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+g2n.model -DEV=xip
-Q=/cgn2_1/USPTO.epool_p/US09857581/rnat_15122005_083136_19383/app_query.fasta.1.711
-DB=Issued_Patents_NA -OPMT=fastap -SUFFIX=rnt -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCLIGN=200 -THR SCORE=pct -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09857581.@CEN.1.1.290 @rnat_15122005_083136_19383 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOC=100 -LONCLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA.*

1: /cgn2_6/ptodata/1/ina/1.COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5.COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*
5: /cgn2_6/ptodata/1/ina/H.COMB.seq.*
6: /cgn2_6/ptodata/1/ina/PCUS.COMB.seq.*
7: /cgn2_6/ptodata/1/ina/PP.COMB.seq.*
8: /cgn2_6/ptodata/1/ina/RE.COMB.seq.*
9: /cgn2_6/ptodata/1/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------------|
| 1 | 2250 | 94.2 | 1824 | 3 | US-08-948-564-13 |
| 2 | 944.5 | 39.5 | 1730 | 3 | US-09-672-785-3 |
| 3 | 943.5 | 39.5 | 1724 | 3 | US-09-672-785-1 |
| 4 | 921.5 | 38.6 | 1770 | 3 | US-09-672-785-7 |
| 5 | 637.5 | 26.7 | 1660 | 3 | US-09-142-108C-16 |
| 6 | 629 | 26.3 | 1488 | 3 | US-09-689-783A-1 |
| 7 | 626 | 26.2 | 1711 | 3 | US-09-142-108C-5 |
| 8 | 625 | 26.2 | 1781 | 3 | US-09-499-302A-1 |
| 9 | 623 | 26.1 | 1748 | 3 | US-09-142-108C-14 |

| | | | | | | |
|----|-------|------|------|---|--------------------|-------------------|
| 10 | 618.5 | 25.9 | 1762 | 3 | US-08-881-784-5 | Sequence 5, Appl |
| 11 | 618.5 | 25.9 | 1762 | 3 | US-09-292-768-1 | Sequence 1, Appl |
| 12 | 618.5 | 25.9 | 1762 | 3 | US-09-292-768-65 | Sequence 65, Appl |
| 13 | 618 | 25.9 | 1806 | 3 | US-09-351-229-3 | Sequence 3, Appl |
| 14 | 616.5 | 25.8 | 1665 | 3 | US-08-881-784-8 | Sequence 8, Appl |
| 15 | 616.5 | 25.8 | 1665 | 3 | US-09-292-768-3 | Sequence 3, Appl |
| 16 | 616.5 | 25.8 | 1665 | 3 | US-09-292-768-67 | Sequence 67, Appl |
| 17 | 616.5 | 25.8 | 1789 | 3 | US-09-142-108C-1 | Sequence 1, Appl |
| 18 | 616.5 | 25.8 | 1665 | 3 | US-09-292-768-69 | Sequence 69, Appl |
| 19 | 613.5 | 25.7 | 1762 | 3 | US-09-292-768-63 | Sequence 63, Appl |
| 20 | 606.5 | 25.4 | 1762 | 3 | US-09-172-339-5 | Sequence 5, Appl |
| 21 | 600.5 | 25.1 | 1515 | 3 | US-09-292-768-5 | Sequence 5, Appl |
| 22 | 593 | 24.8 | 1815 | 3 | US-09-142-108C-18 | Sequence 18, Appl |
| 23 | 590.5 | 24.7 | 1737 | 3 | US-09-142-108C-3 | Sequence 3, Appl |
| 24 | 590 | 24.7 | 1824 | 3 | US-09-142-108C-20 | Sequence 20, Appl |
| 25 | 583 | 24.4 | 1657 | 3 | US-08-948-564-11 | Sequence 11, Appl |
| 26 | 578.5 | 24.2 | 1722 | 3 | US-09-033-055A-1 | Sequence 1, Appl |
| 27 | 574 | 24.0 | 1757 | 2 | US-08-313-075A-49 | Sequence 49, Appl |
| 28 | 574 | 24.0 | 1757 | 3 | US-09-142-108C-26 | Sequence 26, Appl |
| 29 | 571.5 | 23.9 | 2174 | 3 | US-08-606-505B-63 | Sequence 63, Appl |
| 30 | 571.5 | 23.9 | 2174 | 3 | US-09-616-990-63 | Sequence 63, Appl |
| 31 | 567 | 23.7 | 1667 | 3 | US-09-142-108C-22 | Sequence 22, Appl |
| 32 | 566.5 | 23.7 | 1665 | 2 | US-08-313-075A-29 | Sequence 29, Appl |
| 33 | 565.5 | 23.7 | 1893 | 2 | US-08-532-065B-1 | Sequence 1, Appl |
| 34 | 564.5 | 23.6 | 1927 | 3 | US-08-606-505B-64 | Sequence 64, Appl |
| 35 | 564.5 | 23.6 | 1927 | 3 | US-09-616-990-64 | Sequence 64, Appl |
| 36 | 563.5 | 23.6 | 1812 | 2 | US-08-313-075A-37 | Sequence 37, Appl |
| 37 | 563.5 | 23.6 | 1824 | 3 | US-08-606-505B-1 | Sequence 1, Appl |
| 38 | 563.5 | 23.6 | 1824 | 3 | US-09-616-990-1 | Sequence 1, Appl |
| 39 | 561.5 | 23.5 | 1764 | 3 | US-09-947-027-3 | Sequence 404, App |
| 40 | 559.5 | 23.4 | 2013 | 3 | US-09-615-192A-404 | Sequence 2, Appl |
| 41 | 557.5 | 23.3 | 1634 | 3 | US-09-126-420A-2 | Sequence 1, Appl |
| 42 | 556.5 | 23.3 | 1737 | 3 | US-09-126-420A-1 | Sequence 1, Appl |
| 43 | 556.5 | 23.3 | 1838 | 2 | US-09-091-4632-1 | Sequence 1, Appl |
| 44 | 556.5 | 23.3 | 1838 | 3 | US-09-387-663-1 | Sequence 1, Appl |
| 45 | 556.5 | 23.3 | 1838 | 3 | US-09-214-139B-2 | Sequence 2, Appl |

ALIGNMENTS

RESULT 1
US-08-948-564-13
; Sequence 13, Application US/08948564
; Patent No. 6121512
; GENERAL INFORMATION:
; APPLICANT: Simmsky, Balaze
; APPLICANT: Dewey, Ralph E.
; APPLICANT: Corbin, Frederick T.
; TITLE OF INVENTION: No. 6121512el Cytochrome P-450 Constructs and
; TITLE OF INVENTION: Methods of Producing Herbicide-Resistant Transgenic Plants
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Virginia C. Bennett
; STREET: PO Box 37428
; CITY: Raleigh
; STATE: No. 6121512ch Carolina
; COUNTRY: USA
; ZIP: 27627
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/948,564
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Bennett, Virginia C.
; REGISTRATION NUMBER: 37,092
; REFERENCE/DOCKET NUMBER: 5051-409
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-854-1400

```

; TELEFAX: 919-854-1401
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1824 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 54..1616
; US-09-857-581b-66 (1-521) x US-08-948-564-13 (1-1824)

Alignment Scores:
Pred. No.: 1,32e-300 Length: 1824
Score: 2250.00 Matches: 451
Percent Similarity: 86.56% Conservative: 0
Best Local Similarity: 86.56% Mismatches: 70
Query Match: 94.18% Indels: 0
DB: Gaps: 0

US-09-857-581b-66 (1-521) x US-08-948-564-13 (1-1824)
QY 1 MetLeuLeuGluLeuAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeuArgPro 20
DB 54 ATGTTGCTTGAACCTTGCACCTGTTTATTGTTTGGCTCTGTTTGCACCTTGGCTCC 113
QY 21 ThrPro***Ala***SerIysAlaLeuArgHisLeuProAsnProProSerPro***Pro 40
DB 114 ACACCCACCTGCAGAAATCAAAAGACATTCGCCATCTCCAAACCCACCAACCCAAAGCCCT 173
QY 41 ArgLeuProPheIleGlyHis***HisLeuLeuLysAspLysLeuLeuHisIleTyrAla*** 60
DB 174 CGCTTCCTCCCTTCATAGACACCTTCATCTCTTAAAGACAACTTCTCCACTACGACATC 233
QY 61 IleAspLeuSerLysLysHisGlyProLeuPheSer****PheGlySerMetProThr 80
DB 234 ATGACACTCTCCAAAAAAGATGGTCCCTTATTCCTCTCACTTGGCTCCATGCCAAC 293
QY 81 ValValAlaSerThrProGluLeuPheLeuPheLeuGln****GluAlaThrSer 100
DB 294 GTGTGTGCTCCACACACGAAATGTTCAAGCTCTCTCCAAACGACGAGGCAACTCTCC 353
QY 101 Phe***ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp*****ValAla 120
DB 354 TTCAACACAAAGTTCCAAACCTCAGCCATTAAGACGCTCACTAGTAAGCTCAGTGGCC 413
QY 121 *****Pro***GlyProTyrTyr***PheValArgLysLeuIleMetAsnAspLeu** 140
DB 414 ATGTTTCCCTTGGACCTTACTGGAAGTTCGTAGAGAACTCATCAAGAACGACCTTCCC 473
QY 141 AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***Leu 160
DB 474 AAGGCACACCACTGTAAACAAGTTGAGGCTTTTGAGGACCCCAACAGACCCCAAGTTCCT 533
QY 161 Arg***MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGluGluLeuLeu 180
DB 534 AGGGTTATGGCCCAAGGCGACAGGCGACAGAAAGCCCTTGACTTGAAGCGAGAGCTTCTG 593
QY 181 LysTyr***AsnSerThr***SerMetMet***LeuGlyGluAlaGlnGluIleArgAsp 200
DB 594 AATATGACCAACAGCAACATCTCATATGATGTCGGCAGAGGTGAGGATCAAGAGAC 653
QY 201 IleAlaArgGluValLeuLysIle***GlyGluTyrSerLeuThrAspPheIle***Pro 220
DB 654 ATGCTCTCGCAGAGGTTCTTAAGATCTTTGGCGAAATACAGCTCACTGACTCATCTGGCCA 713
QY 221 LeuLys***LeuLysValGlyLysTyrGluLysArgLysLeuAspIleLeuAsnLysPhe 240
DB 714 TTGAAGCATCTCAAGGTTGAGAAATATGAGAAAGGATCAAGACATCTTGAACAGTTC 773
QY 241 AspProValValGluArgValIleLysLysArgArg***IleValArgArgArg***Asn 260
DB |||||

```

```

DB 774 GACCTGTGCTGTAAGAGGTCATCAAGAAAGCCCGTGAAGATGCTGAGAGAGAAAGAAC 833
QY 261 GlyGlu*****GluGlyGlu***SerGlyVal***LeuAspThrLeuGlnIlePheAla 280
DB 834 GGAAGAGTTGTTGAGGGTGAAGGTCAAGCGGGGTTTCTTCTGACACTTGTGTAATTCGCT 893
QY 281 GluAspGluThr***GluIleLysIleThrLys*****Ile***GlyLeuValValAsp 300
DB 894 GAGATGAGACCATGAGATCAAAATCAACCAAGACACATGAGAGGCTTGTGTGCAGC 953
QY 301 ***PheSerAlaGly***AspSerThrAla*****ThrGluTyrAlaLeuAlaGluLeu 320
DB 954 TTTTCTCGGACAGAAACAGACTCCACAGCGGTGCGAAGAGGTGGGCATTTGCAGAACTTC 1013
QY 321 IleAsnAsnPro***ValLeu*****AlaArgGluGlu***TyrSerValValGlyLys 340
DB 1014 ATCAACAAATCCTAAGGTGTTGAAAAGGCTCGTAGAGAGCTTACAGTGTGGGAAAG 1073
QY 341 Asp***LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLys 360
DB 1074 GACAGACTTGTGACGCAAGTTGACACTCAAACTTCTTACATTAGACCAATCGTGAAG 1133
QY 361 GluThrPheArgMetHisProProLeuProValValLysArgLysCys**GluGluCys 380
DB 1134 GAGACATTCGCGATGACACCCGACCTCCAGTGTGCAAAAGAGTGCACAGAGAGTGT 1193
QY 381 ***IleAsnGly***Val***ProGluGluValAlaLeu*****PheAsnValTyrGluVal 400
DB 1194 GAGATTAAATGAGATGTGATCCACAGGGAGCATTTGATTTCTTCAATGTAAGCAAGTA 1253
QY 401 Gly***Asp***LysTyrTyrAspArgProSerGlu***ArgProGluArgPheLeuGlu 420
DB 1254 GGAAGAGACCCCAATACAGGACAGACCATGGAGTTCGTCCTGAGAGGTTCTTAGAG 1313
QY 421 Thr***AlaGluGlyGluAla*****LeuAspLeuArgGly***HisPheGlnLeuLeu 440
DB 1314 ACAGGGGCTGAAGGGGAGACAGGGCTCTTGATCTTGAAGGAGCAAACTTTCAACTTCTC 1373
QY 441 ProPheGlySerGlyArg***MetCysProGluVal***LeuAlaThrSerGly***Ala 460
DB 1374 CCATTGGGTCTGGGAGGAGAAATGTGCTCGAGATCAATCTTGCTTCTCGGAAATGGCA 1433
QY 461 ThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGln 480
DB 1434 ACACCTTCTGCACTCTTATTCAGTGTCTCGACTTGCAGTTCGAAGTGTGGGTCCACAAGACAG 1493
QY 481 IleLeuLysGly***AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValPro 500
DB 1494 ATATTGAAGGGTGTGACCCCAAGTTAGCATGAAAGAGAGAGCCGCTCACTGTTCACA 1553
QY 501 ArgAlaHisSerLeuValCysValProLeuAlaArgIleGlyValAlaSerLysLeuLeu 520
DB 1554 AGGCACATATGCTGTGTGTGTTCATTGCAAGGATCGGGGTGCATCTTAACCTCTT 1613
QY 521 Ser 521
DB 1614 TCT 1616

RESULT 2
US-09-672-785-3
; Sequence 3, Application US/09672785
; Patent No. 6596927
; GENERAL INFORMATION:
; APPLICANT: Mizutani, Masako
; APPLICANT: Kasumi, Takaaki
; APPLICANT: Ayabe, Shin-ichi
; APPLICANT: Akashi, Tomoyoshi
; TITLE OF INVENTION: Genes Coding for Flavone Synthases
; FILE REFERENCE: 001560-383
; CURRENT APPLICATION NUMBER: US/09/672,785
; PRIOR APPLICATION NUMBER: 2000-09-29
; PRIOR FILING DATE: PCT/JP00/04379
; PRIOR FILING DATE: 2000-01-30

```


PRIOR APPLICATION NUMBER: JP 11-22427
 PRIOR FILING DATE: 1999-01-29
 NUMBER OF SEQ ID NOS: 8
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 7
 LENGTH: 1770
 TYPE: DNA
 ORGANISM: *Perilla frutescens*
 FEATURE:
 OTHER INFORMATION: Nucleotide sequence encoding a protein having an
 OTHER INFORMATION: activity to directly convert flavanone to flavone
 OS-09-672-785-7

| | |
|------------------------|-----------|
| Alignment Scores: | |
| Pred. No.: | 8.35e-117 |
| Score: | 921.50 |
| Percent Similarity: | 57.46% |
| Best Local Similarity: | 38.85% |
| Query Match: | 38.57% |
| DB: | 3 |
| | |
| Length: | 1770 |
| Matches: | 190 |
| Conservative: | 91 |
| Mismatches: | 183 |
| Indels: | 25 |
| Gaps: | 8 |

US-09-857-581B-66 (1-521) x US-09-672-785-7 (1-1770)

[illegible]

```

Db      804 GCGGCGGGGAGACCAAGATTCTTGTGACATGTTCTCGACATTAATGAGACGGGAAA 863
QY      285 ***GluLeuLysIleThrIys*****Ile***GlyLeuValAlaasp***PheSerAla 304
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      864 GCCGAGGTAAATTCAACGAGGACGACATCTCAAGAGCTTTGATTTCTGGAATTTCTTACCGCC 923
QY      305 Gly***AspSerThrAla*****ThrGluTrpAlaLeuAlaGluLeuIleAsnAspPro 324
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      924 GGCACCCAGACGACGGGATCGTGTGTGAATGGGCGCATGACAGAAAGATCAACATCCA 983
QY      325 ***ValLeu*****AlaArgGluGlu***TyrSerValAlaGlyLysasp***LeuVal 344
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      984 AATGTGTGAAGAAAGCTCAAGAAAGATTGCCAACATCTCGATTTCGACAGAAATCTCG 1043
QY      345 AspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLysGluThrPheArg 364
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      1044 CAAGAAATCCGACGGCCCAAAATCTGCCTTACCTTCAACCCCTCATCAAGAAACATTCGCG 1103
QY      365 MetHisProProLeuProValValLysArgLysCys***GluGluCys***IleAsnGly 384
      ::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      1104 CTCACACCTCCAAATCCCAATGCTGGCGAGAGAAATCGATCTCCGACTGCTGATCGACGCG 1163
QY      385 ***Val***ProGluGluAlaLeu*****PheAsnValTrpGluValGly***Asp** 404
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      1164 TACATGATTCGCGCAACACGCTCTCTTGTCTGACACCTCTGTGTCATGCGGCGGAACCT 1223
QY      405 LysTyrTrpAspArgProSerGlu***ArgProGluArgPheLeuGluThr**AlaGlu 424
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      1224 AAAATCTGGGACTACCCGAGCGGCTTCAGCGGAGGTTTCTGGAAG----- 1274
QY      425 GlyGluAla*****LeuAspLeuArgGly***HisPheGlnLeuLeuProPheGlySer 444
      ::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      1275 ---GAAAAAGCGCGCATCGATGTTAAAGGGGAGCATTTTGACGTCACCGTTCGGAACG 1331
QY      445 GlyArg***MetCysProGlyVal***LeuAlaThrSerGly***AlaThrLeuLeuAla 464
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      1332 GCGCGAGAGAGCGCTGCCAGGGATCTTTTACCCATTACAGAGGCGTGCATCATATAATGCG 1391
QY      465 SerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGlnIleLeuLysGly 484
      :::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      1392 ACGATGATTCATGTTGATTGGAAGCTG-----CCGACGCG----- 1430
QY      485 **AspAlaLysValSerMetGluGluArgAlaGlyLeuThrValProArgAlaHisSer 504
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      1431 ---TCGGCGCATGTTGATATGCGAGAACCGCCAGGGCTCACGAGACCGGACGAGAT 1487
QY      505 LeuValCysValProLeuAlaArgIle 513
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      1488 TTGTTTTCGCGTGTGTCGCCGAGATT 1514

RESULT 5
US-09-142-108C-16
/ Sequence 16, Application US/09142108C
/ Patent No. 6774285
/ GENERAL INFORMATION:
/ APPLICANT: Bruggliera, Filipa
/ APPLICANT: Holton, Timothy A.
/ APPLICANT: Michael, Michael Z.
/ TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOID PATHWAY ENZYMES
/ FILE REFERENCE: 11658
/ CURRENT APPLICATION NUMBER: US/09/142.108C
/ PRIOR FILING DATE: 1998-09-01
/ PRIOR APPLICATION NUMBER: P8186
/ NUMBER OF SEQ ID NOS: 45
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 16
/ LENGTH: 1660
/ TYPE: DNA
/ ORGANISM: Chrysanthemum
/ FEATURE:
/ NAME/KEY: CDS

```

```

LOCATION: (4) .. (1530)
US-09-142-108C-16

Alignment Scores:
Pred. No.: 1,496-77 Length: 1660
Score: 637.50 Matches: 162
Percent Similarity: 49.81% Conservative: 101
Best Local Similarity: 30.68% Mismatches: 208
Query Match: 26.68% Indels: 57
DB: 3 Gaps: 14

US-09-857-581B-66 (1-521) x US-09-142-108C-16 (1-1660)

QY 5 LeuAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeuArgProThrPro***Ala 24
DB 34 CTGATCTCTGGG---TCAGTACTCTATGATTTCTTAACCTTA----- 72
QY 25 ***SerLyAlaLeuArgHisLeuProAsnProProSerPro***Pro-----Arg 41
DB 73 AGTTGACGTAAATCCGCCAGACTCCACCCGGCCAAACACCATGGCTATAGTCGGGAAAC 132
QY 42 LeuProPhe11eGlyHis***HisLeuLeuLysAspLysLeuLeuHisTyrAla***Ile 61
DB 133 TTAACCAACACCTTGGC-----CCAAATCCCAACACCAACGACTCGCG 171
QY 62 AspLeuSerLysHisGlyProLeuPheSer*****PheGlySerMetProThrVal 81
DB 172 GCCTTAGCCAGAAAGTACGGCCATTGATGCACCTCGCGCTCGGTCGTGACGCGTT 231
QY 82 ValAlaSerThrProGluLeuPheLysLeuPheLeuGln*****GluAlaThrSerPhe 101
DB 232 GTGGCCGCGTCCTCTCCGATGCGACACTTTTAAAGTTCACACGCA---AATTTT 288
QY 102 ***ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp-----ValAla 120
DB 289 GCTAGTAGCGCCGCAAAATCTGGCGCGAAACATGTGCGCGTAAATATATCAGATCTTGG 348
QY 121 *****Pro***GlyProTyrTrp***PheValArgLysLeuLysLeuAsnAspLeu*** 140
DB 349 TTTCGACCTTATGATGTCAGAGTGGCGTTTGAAGAAATTTGTCGCGCCATTGTTT 408
QY 141 AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***Leu 160
DB 409 TCTGCTAAAGACACTTATGATTTTTCGTCATGTCGACAGAGAGTACAGACGCTTAAC 468
QY 161 Arg***MetAlaGln***AlaGluAla***LysProLeuAsp***ThrGluGluLeu 180
DB 469 CCGGTACTACTGAGTGTGAAACTCA-----CCGGTACAGCTTGGCCAACTAATTAC 522
QY 181 LysTrp***AsnSerThr***SerMetMet***LeuGly----- 193
DB 523 GTGTGTCACCAAAACGCTTATGACAGCGGTATATGTTAGGTGAGAGATTTCGAGACGGA 582
QY 194 -----GluAlaGluGlnIleArgAspIleAlaArgGluValLeuLysIle***Gly 210
DB 583 ATTGACAGTCCACCATGATGCTCAAGAATATGTAAGTAAATGATTAAGCAGGA 642
QY 211 GluTyrSerLeuThrAspPhe11e***ProLeuLys***LeuLysValGlyLysTyrGlu 230
DB 643 GAATTTAAACCTTGATGACTTATTCCTGACTTACCTATTCGACCTACCAAGCATTACT 702
QY 231 LysArgIleAspLysIleLeuAsnLysPheAspProValAlaGluArgValIleLysLys 250
DB 703 AAAAAATGAAGAAGCTTCATGTTGGTGCATTCATTTCTTGAATGAAGTGTGAGAG 762
QY 251 ArgArg***IleValArgArg***AsnGlyGlu***GluGlyGlu***SerGly 270
DB 763 CATAAAACG-----GCACCTGCTGGTGGGTGCATACT 795
QY 271 Val***LeuAspThrLeuLeuGluPheAlaGluAspGluThr***Glu---IleLysIle 289
DB 796 GATTCTGTGACGCGTTGATTCATCTTAAAGATGATGCTGATATTTGAAGGTGAGAGCTT 855

```

```

QY 290 ThrLys*****Ile***GlyLeuValValAsp***PheSerAlaGly***AspSerThr 309
DB 856 ACAGATACATGAATCAAAAGCTTTGCTTGAATTTATTTGCTGCGGGAACAAGACATCC 915
QY 310 Ala*****ThrGluTrpAlaLeuAlaGluLeuIleAsnAsnPro***ValLeu***** 329
DB 916 TCTAGTACAGTGAATGGGCAATAGCCGAATCATTCATTCACCAAAATATTAAAAACA 975
QY 330 AlaArgGluGlu***TyrSerValValGlyLysAsp***LeuValAspGluValAspThr 349
DB 976 GCCCGAAGAAGATAGACCGCTGATGTTGTCAGACCGGCTTGTACAGAAATTTGACCTTG 1035
QY 350 GlnAsnLeuProTyrIleArgAlaIleValLysGluThrPheArgMetHisProLeu 369
DB 1036 AGCCAACTAAACATACCTCCAGGCTTGTGAAGAAGAGTGTTAAGCTTCACCTTCACG 1095
QY 370 ProVal---ValLysArgLysCys***GluGluCys***IleAsnGly***Val***Pro 388
DB 1096 CCACCTCCTTACCAAGAAATATCATCCGAGATGTGAGGTGATGATTAATATCCCT 1155
QY 389 GlnGluAlaLeu*****PheAsnValTrpGlnValGly***Asp***LysTyrTrpAsp 408
DB 1156 AAGGATCCACACTCTCTGTTACGTCGTGGCCATTGCCGACACCCAAAATGTGGCG 1215
QY 409 ArgProSerGlu***ArgProGluArgPheLeuGluThr***AlaGluGlyGluAla*** 428
DB 1216 GATCCTCTGAATTTAAGGCTTCTCGTTTAA-----CCCGGGGAAGAAAGCC 1266
QY 429 ***LeuAspLeuArgGly***HisPheGlnLeuLeuProPheGlySerGlyAla***Met 448
DB 1267 GGTGCTGATGATTAGGGGAATGATTTTGAAGTATATCAATTTGGGCGACAGACGAAGATT 1326
QY 449 CysProGlyVal***LeuAlaThrSerGly***AlaThrLeuLysLeuIleGln 468
DB 1327 TGTGCGGATTAAGCTTACGCTTGAAGATGTCACATGCTCATTTGCAACATTTGTCGA 1386
QY 469 CysPheAspLeuGlnVal-----LeuGlyProGlnGlyGlnIleLeuLysGly*** 485
DB 1387 ACTTTGATTTGGAATGTGGCTAAGCGTTAAGCCGAG----- 1425
QY 486 AspAlaLysValSerMetGluAlaArgAlaGlyLeuThrValProArgAlaHisSerLeu 505
DB 1426 -----ATGCTCAACATGGAAGAAGGTATGATGATGATCCCTTCAACGCGCTGACCTTG 1479
QY 506 ValCysValProLeuAlaArgIle 513
DB 1480 ATGCTTACCCGGAAGCGAGTTA 1503

RESULT 6
US-09-689-783A-1
/ Sequence 1, Application US/09689783A
/ Patent No. 6605469
/ GENERAL INFORMATION:
/ APPLICANT: KANG, JEONG-GU
/ APPLICANT: PARK, CHUNG-MO
/ TITLE OF INVENTION: NUCLEIC ACID MOLECULE ENCODING A CYTOCHROME P450 HYDROXYLASE IN
/ TITLE OF INVENTION: BRASSINOSTEROID BIOSYNTHESIS IN PLANTS
/ FILE REFERENCE: 107572
/ CURRENT APPLICATION NUMBER: US/09/689,783A
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 1
/ LENGTH: 1488
/ TYPE: DNA
/ ORGANISM: Pisum sativum
US-09-689-783A-1

Alignment Scores:
Pred. No.: 1,896-76 Length: 1488
Score: 629.00 Matches: 154
Percent Similarity: 49.79% Conservative: 87
Best Local Similarity: 31.82% Mismatches: 199

```


Query Match: 26.33% Indels: 44
 DB: 3 Gaps: 12

US-09-857-581B-66 (1-521) x US-09-689-783A-1 (1-1488)

```

QY 35 ProProSerPro***ProArgLeuProPheIleGlyHis***HisLeuLeuLysAspLys 54
DB 106 CCACCAAGGCCCAAAACCA---TGGCCCATTAATAGGAACCTTCAACCTTAT---GGAACC 159
QY 55 LeuLeuIleTyAla***IleAspLeuSerLysLysGlyProLeuPheSer***** 74
DB 160 CTCACCAACCAATCCCTCCATGGGCTCACCACCAAAATATGACCTATTAATGACATCATG 219
QY 75 PheGlySerMetProThrValValAlaSerThrProGluLeuPheLysLeuPheLeuGln 94
DB 220 TTCGGCTCCAAAGCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 279
QY 95 *****GluAlaThrSerPhe***ThrArgPheGlnThrSerAla***Arg***LeuThr 114
DB 280 ACCCAGCAGCAACG---TTAGCCGGCCGACCCCAAAATTCCTGCGGAAATACACAACT 336
QY 115 TyrAsp-----ValAla*****Pro***GlyProTyTrp***PheValArgLys 133
DB 337 TATTAATCTACTGACATTAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 396
QY 134 LeuIleMetAsnAspLeu***AsnAlaThrThrValAsn***LeuArgProLeuArgThr 153
DB 397 ATGTGCTATTAATTAATTTTGTAGTGCAGAAACGCTTGTAGCTTATGATCATTAAGAAA 456
QY 154 GlnGlnIleArgLys***LeuArg***MetAlaGln***AlaGluAla***LysProLeu 173
DB 457 CAAGAGTACATGCTTTTTCATGACGAACTCTTGATTTCAAGAAC-----AAACATT 510
QY 174 Asp***ThrGluGluLeuLeuLysTrp***AsnSerThr***SerMetMet***LeuGly 193
DB 511 TTGTTGAAGACCATTTTCAAGTTTGAAGTTTGAAGTTTGAAGTTTGAAGTTTGAAGTTTGA 570
QY 194 -----GluAlaGluGluIleArgAspIle 201
DB 571 AGGAATATCTAGAGAGTTGAAATCTTATTTCTCCGATGAGTTTGAAGATATG 630
QY 202 AlaArgGluValLeuLysIle***GlyGlnTySerLeuThrAspPheIle***ProLeu 221
DB 631 TTGGATGAGTTGTTTGTCTTAATGCGATCTTAAATTTGGGAGATTTTATCTTGGATT 690
QY 222 Lys***LeuLysValGlyLysTyGluLysArgLysLeuAspIleLeuAsnLysPheAsp 241
DB 691 CATTTCTTAGATTTTCAAGGATATGTAAGAGGATTTGAGTAAAGATTTGAT 750
QY 242 ProValValGluArgValIleLysLysArgArg***IleValArgArgArg***AsnGly 261
DB 751 GGATTTATGGAACATGTTGTTGAGGAACAT-----ATTGAAGAAAGAAAGCGTTAAG 804
QY 262 Glu*****GluGlyGlu***SerGlyVal***LeuAspThrLeuLeuGluPheAlaGlu 281
DB 805 GATTAATGTGCTAGAT-----ATGGTGAATGTTCTTTGCAACTTGTGAG 852
QY 282 AspGluThr***GluIleLysIleThrLys*****Ile***GlyLeuValValAsp*** 301
DB 853 GATCTGATCTTGAAGCTTGAAGCTTGAAGCATGCTGTAAAGCTTTTACTCAGACACTG 912
QY 302 PheSerAlaGly***AspSerThrAla***ThrGluTrpAlaLeuAlaGluLeuIle 321
DB 913 ATACAGAGGAGACAGAGCTCAGACATGACATGATGCGCATTCGACACTATA 972
QY 322 AsnAsnPro***ValLeu***AlaArgGluGlu***TyrSerValValGlyLysAsp 341
DB 973 AGAAACCAAGAAATCTTCAAGAAAGCAAGAGCAACATGACAGATATGAGAGAGAA 1032
QY 342 ***LeuValAspGluValAspThrGlnAsnLeuProTyxIleArgAlaIleValLysGlu 361
DB 1033 AGATGGTTGAAGAGAAACATTTGCTATCTTATGTTATGATGCAATTCCTTAAGAA 1092
  
```

```

QY 362 ThrPheArgMetHisProProLeuPro---ValValLysArgLysCys***GluGluCys 380
DB 1093 ACAATGACATCTTCAACCAAGTGGACCAATGTTAGTACCAAGAGAGATGAGAAATTC 1152
QY 381 ***IleAsnGly***Val***ProGluGlyAlaLeu*****PheAsnValTrpGlnVal 400
DB 1153 AATATCAATGATATGATATTCACAAAGGCTTTGATTTCTTTAATCTTGAACATTT 1212
QY 401 Gly***Asp***LysTyTrpAspArgProSerGlu***ArgProGluArgPheLeuGln 420
DB 1213 GCAAGAGTTTAAATGTTTGGATATTCAAATGAGTTTATGCCAGAGAGTTTCTT 1269
QY 421 Thr***AlaGluGlyGluAla*****LeuAspLeuArgLys***HisPheGlnLeuLeu 440
DB 1270 -----GTAAGATATATGATGTAAGAGCAATGATATGATGATGTTG 1311
QY 441 PropheGlySerGlyArg***MetCysProGlyVal***LeuAlaThrSerGly***Ala 460
DB 1312 CCATTTGGTGTGTGTAAGAGATGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1371
QY 461 ThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGln 480
DB 1372 TCAAGTTTGGCTAAATTTGTTGATGATGATTTAATGAGATTCG----- 1413
QY 481 IleLeuLysGly***AspAlaLys-----ValSerMetGluGluArgAlaGlyLeu 497
DB 1414 -----AGTATGATGATGTAAGAAAGAGATTTGAATATGAGAGATTTTGGGCTT 1464
QY 498 ThrValProArg 501
DB 1465 TCTACACCTAAG 1476
  
```

RESULT 7
 US-09-142-108C-5
 ; Sequence 5, Application US/09142108C
 ; Patent No. 6774285
 ; GENERAL INFORMATION:
 ; APPLICANT: Bruggliera, Philippa
 ; APPLICANT: Holton, Timothy A.
 ; APPLICANT: Michael, Michael Z.
 ; TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOID PATHWAY ENZYMES
 ; TITLE OF INVENTION: AND USES THEREFOR
 ; FILE REFERENCE: 11658
 ; CURRENT APPLICATION NUMBER: US/09/142,108C
 ; CURRENT FILING DATE: 1998-09-01
 ; PRIOR APPLICATION NUMBER: PNB386
 ; PRIOR FILING DATE: 1996-03-01
 ; NUMBER OF SEQ ID NOS: 45
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 5
 ; LENGTH: 1711
 ; TYPE: DNA
 ; ORGANISM: Antirrhinum majus
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (91)..(1629)
 ; US-09-142-108C-5

Alignment Scores:
 Pred. No.: 6,12e-76
 Score: 626.00
 Percent Similarity: 47.94%
 Best Local Similarity: 30.34%
 Query Match: 26.20%

| DB: | 3 | Gaps: | 14 |
|---|---|-------|----|
| US-09-857-581B-66 (1-521) x US-09-142-108C-5 (1-1711) | | | |
| QY 1 MetLeuLeuGluLeuAlaLeuGlyLeu***ValLeuAlaLeuPhe***HisLeuArgPro 20 | | | |
| DB 145 TTATTTGGTCCATGATCTTATTAATGAGGTTCTTCTTATTAATCTTCTCTC----- 198 | | | |
| QY 21 ThrPro***Ala***SerLysAlaLeuArgHisLeuProAsnProProSerPro***Pro 40 | | | |

```

Db 199 -----AACAAAAAGTAAGCCACCTGACCGAAGCCATGGCCC 243
Qy 41 -----ArgLeuProPheIleGlyHis**HisLeuLeuLysAspLysLeuLeuHis 57
Db 244 ATCTGCGAAGAACTGACATCTTGGCGGAAGCCC-----CAC 282
Qy 58 TyrAla***IleAspLeuSerLysLysHisGlyProLeuPheSer*****PheGlySer 77
Db 283 CAGTCATGAGCGGCGCTGGCAGCGGTGACGCGCCCTTAATTATCTGTAAGATGGGCTTT 342
Qy 78 MetProThrValValAlaSerThrProGluLeuPheLysLeuPheLeuGln*****Glu 97
Db 343 GTGCATGTGTGTGTGGCTCTCTCAGCATCCGTTGGCGAAGAAATTTCTGAAGGTCATGAC 402
Qy 98 AlaThrSerPhe***ThrArgPheGlnThrSerAla***Arg***LeuThrTyrAsp--- 116
Db 403 GCA---AACTTCTCGCAGCGGCTCCCAATTCCGGTGCAGAAACACGTGGCTTACACATAT 459
Qy 117 *****ValAla*****Pro***GlyProTyrTrp***PheValArgLysLeuIleMet 136
Db 460 CAGGACTGTGTCTTCTCTCTTATGGCCACGCTGGCGATGCTCAGAAATCTGTGCA 519
Qy 137 AsnAspLeu***AsnAlaThrThrValAsn***LeuArgProLeuArgThrGlnGlnIle 156
Db 520 CTCACCTCTCTTCCGCGCAAGCCTTGAAGACTTCACACAGCTCAGACAGATGAGTG 579
Qy 157 ArgLys***LeuArg***MetAlaGln***AlaGluAla***LysProLeuAsp***Thr 176
Db 580 GGGATCCTCACTCGCTTCTTACGATGCAAGCAAGCAAG-----CCGTTGAATTAAGG 633
Qy 177 GluGluLeuLeuLysTrp***AsnSerThr***SerMetMet***LeuGly----- 193
Db 634 CAGATATGAACACATGCCGCCACCAATGCAATGACGGGTGTATGTTGGTCAACCGCG 693
Qy 194 -----GluAlaGluGluIleArgAspIleAlaArgGluValLeuLys 207
Db 694 GTTGCACAGCAGACTCAAAAGCGGAGAGTTTAAGGCATGTAGTGAGTTGATGAGTA 753
Qy 208 Ile***GlyGluTyrSerLeuThrAspPheIle***ProLeuLys***Leu----- 224
Db 754 TTAGCTGTGTGTGTTCACTTACCTTGAATTTATCCACCTCTTAAATAATGATCTTCA 813
Qy 225 -----LysValGlyLysTyrGluLysArgIleAspAspIleLeuAsnLysPhe 240
Db 814 GGTGTATTGCTAAGATGAAGAAGCTTCACTTGCATTCGATTCGTTCTTGAAGTAAH--- 870
Qy 241 AspProValValGluArgValIleLysLysArgArg***IleValArgArgArg***Asn 260
Db 871 -----ATCCTTGAAGACCAAGATC 891
Qy 261 GlyGlu*****GluGlyGlu**SerGlyVal**LeuAspThrLeuLeuGluPheAla 280
Db 892 AACAGCTCAGATGAACCAAGAGCCATTCGATTTGTGTAACATGTTAATTTCTTGAAG 951
Qy 281 Glu---AspGluThr***GluIleLysIleThrLys*****Ile***GlyLeuValVal 299
Db 952 GAGCGTGAATGCCAGAGGAGGAGGCTCAGCAGCTGTAAGAAATTAAGCGTTGCTCTTG 1011
Qy 300 Asp***PheSerAlaGly**AspSerThrAla*****ThrGluTrpAlaLeuAlaGlu 319
Db 1012 AACTTGTTCCTGACAGAACTGACACACATCAAGACCTGTGAATGTGTCATAGCTGAG 1071
Qy 320 LeuIleAsnAsnPro**ValLeu*****AlaArgGluGlu**TyrSerValValGly 339
Db 1072 TTAGTTCGACATCTTAATCTTGGCCAAAGTCCAAATAAACTCGACTCTGTGTGTGGT 1131
Qy 340 LysAsp***LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleVal 359
Db 1132 AAGAATCGGTGTGGAAGGCTGATCTGGCCGATATCAATTCCTCCAAAGCGGTGTC 1191
Qy 360 LysGluThrPheArgMetHisProProLeuProVal---ValLysArgLysCys***Glu 378

```

```

Db 1192 AAGAAATATTCGACTCCATCCCTCCACCCGCTCTCCCTACCGAGATCCACATGAG 1251
Qy 379 GlyCys***IleAsnGly***Val***ProGluGluValAlaLeu*****PheAsnValTrp 398
Db 1252 AACTTGAAGTGAATGAATGATCTTGAATCCAAAGGTTGACACTTCTTCAATGTTGG 1311
Qy 399 GlnValGly**Asp***LysTyrTrpAspArgProSerGlu***ArgProGluArgPhe 418
Db 1312 GCAATTCCTCGGAGATCCCAAAATGTGGATGTAACACATGAGATTCGCGCTGAAGATTC 1371
Qy 419 LeuGluThr***AlaGluGlyGluAla*****LeuAspLeuArgGly***HisPheGln 438
Db 1372 TTGAAG-----GGCGGGGAAAAGCCTTAATGTGAGTGAAGGGAATGATTTGCA 1422
Qy 439 LeuLeuProPheGlySerGlyArg**MetCysProGluVal**LeuAlaThrSerGly 458
Db 1423 TTGATTCGTTGAGAGCGGCGGGAAGAAATTTGTGAGAGATAGCTTGAATACCTATG 1482
Qy 459 **AlaThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGluValLeuGlyProGln 478
Db 1483 GTCCAGTTGTTGACAGCAACTTGAACCATGCGTTGACTTGTGATTTG-----GGGAT 1536
Qy 479 GlyGlnIleLeuLysGly***AspAlaLysValSerMetGluGluArgAlaGlyLeuThr 498
Db 1537 GGACAGTTG-----CTGAAAGCTTAAACATGAGAGAAAGCTTATGCGCTGACC 1584
Qy 499 ValProArgAlaHisSerLeuValCysValProLeuAlaArg 512
Db 1585 TTGCAACGAGCTGACCTTGTGTGATGCAAGCAAGCCTTAAG 1626

RESULT 8
US-09-499-302A-1
/ Sequence 1, Application US/09499302A
/ Patent No. 6369212
/ GENERAL INFORMATION:
/ APPLICANT: BOUNG-JUN, OH
/ APPLICANT: MOON, KYUNG KO
/ APPLICANT: YOUNG, SOON KIM
/ TITLE OF INVENTION: A CYTOCHROME P450 GENE HIGHLY EXPRESSED IN THE
/ FILE REFERENCE: 10324/P6443050
/ CURRENT APPLICATION NUMBER: US/09/499,302A
/ NUMBER OF SEQ ID NOS: 10
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1
/ LENGTH: 1781
/ TYPE: DNA
/ ORGANISM: Capsicum annum
US-09-499-302A-1

Alignment Scores:
Pred. No.: 8,95e-76 Length: 1781
Score: 625.00 Matches: 151
Percent Similarity: 49.28% Conservative: 89
Best Local Similarity: 31.01% Mismatches: 211
Query Match: 26.16% Indels: 36
DB: 3 Gaps: 14

US-09-857-581B-66 (1-521) x US-09-499-302A-1 (1-1781)
Qy 35 ProProSerPro**ProArgLeuProPheIleGlyHis**HisLeuLeu-----Lys 52
Db 100 CTCCTCGTCCATG---AAATTACCTTTATTTGAAGCTTACATCTTGGCAGTGCA 156
Qy 53 AspLysLeuLeuHisTyrAla**IleAspLeuSerLysLysHisGlyProLeuPheSer 72
Db 157 GGTCCACTTCCTCATATGAGCGCTAATAAAATCTAGCAAACTTATGCGCGCTCATGAC 216
Qy 73 ****PheGlySerMetProThrValValAlaSerThrProGluLeuPheLysPhe 92
Db 217 TTACGACTGGGGAATTCCTACCGTCATCATTTGTCCTCCGCGAATGCGAAGGAATA 276

```

QY LeuGln*****GluAlaThrSerPhe***ThraArgPheGlnThrSerAla****Arg**** 112

Db CTAATAAATCTACACGAC---CTCGCTTTCGCAACGAGCGCCAACTGTGTGCTGCACATC 333

QY LeuThrLysPhe*****ValAla*****Pro***GlyProTyrTrp***PheVal 131

Db GTCCATTATGATAGTACGATATAGCATTTTCTTCATATAGTGAAATCTGAGAGCAGATT 393

QY ArgLysLeuIleMetAsnAspLeu***AsnAlaThrThrValasn***LeuArgProLeu 151

Db CGTAAATATTGCATACATCGCAACTCCTTAGTGCCAAAGATGGCAAAATCTTTAGCTCAATT 453

QY ArgThrGlnGlnIleArg-----Lys***LeuArg***MetAlaGln***AlaGln 168

Db CGCCAGAGATGAGCTGTCGATGATGATGTCATCTATACGAACCAATGCCAAATTTT----- 507

QY Ala***LysProLeuAsp***ThrGlnGlnLeuLeuLysTrp***AsnSerThr***Ser 188

Db -----CCGCGTCAACCTTACAGACAAATATTTGGTTTACAGTTTGCGTATCTGT 558

QY MetMet***LeuGly-----GluAlaGlnIleArgAspIleAlaArgGlu 204

Db AGATCAGCTCTCGGAAAAATATGTCGACCAACAACAACATGATAATTTCATGAGGAA 618

QY ValLeuLysIle***GlyGluTyrSerLeuThrAspPheIle***ProLeuLys***Leu 224

Db ATAAATATCATTTGACGAGGTGATTTATAGTATTCCTATTTTTCCTACATGAGAAATGCTA 678

QY ---LysValIleGlyLysTyrGlnLysLeuArgIleAspAspIleLeuAsnLysPheAspProVal 243

Db CATGATGTTGGTGGTTCACAAAACATAGATGCTGAAAGCTCATCGTAAATTCAGATGATT 738

QY ValGluArgValIleIleLysLeuArgArg***IleValArgArgArg***AsnGlyGlu*** 263

Db TTGGAAACATGTATGATCATAGACACAA-----CAGATCGAGCGGAGTGGCCAAAG 789

QY ***GlnGlyGln***SerGlyVal**Leu--AspThrLeuLeuGlnPheAlaGlnLysP 282

Db GGTATAGCGCAATTTGGCGGTGAAGATTGTGATCGATGTTTTCCTAGAGGTTTCGAAAGT 849

QY GlnThr***GlnIleLysIleThrLys*****Ile***GlyLeuValValAsp***Phe 302

Db GGAGAAGTTCAAATTTCCATCGACGATGACATATCAATATCAATATTTATGTGACATGTTT 909

QY SerAlaGly***AspSerThrAla*****ThrGluTrpAlaLeuAlaGlnLeuIleAsn 322

Db TCCGCTGGATTCGAAACGTCAATCGACACATATTAATTGGCATTTAGCTGAATGATGAA 969

QY AsnPro***ValLeu*****AlaArgGlnGlu***TyrSerValValGlyLysPhe*** 342

Db AAACCAAGTTCCTAGCAAGGCAACAAGCTGGAAGACAAAGTCTTGAMAGAAAGAAA 10299

QY LeuValAspGlnValAspThrGlnAsnLeuProTyrIleArgAlaIleValLysGlnThr 362

Db GGTTTTCAACAAATTTGATCTTGATGATGAGTTGAAGTACTTGAAGTATGATCAAGAACT 10899

QY PheArgMetHisProProLeuPro---ValValLysArgLysCys***GlnLysCys*** 381

Db CTAAGAGATCACCCCTCCATTTCTCTATTAGTCCCTAGAGATGATGAGAGATCAAG 11499

QY IleasnGly***Val***ProGlnGlnAlaLeu*****PheAsnValTyrGlnValGly 401

Db ATTTGAGCGGTACAAATATACCTTTCAAACTCGACATCATGTTAAAGCATGGCCATTTGA 12099

QY ***Asp***LysTyrLysAspArgProSerGln***ArgProGlnArgPheLeuGlnThr 421

Db CGAGATCCCGAAAGTTGGAGTACCTTGAAAGCTTTTCCCGAGAGATTC----- 12666

QY ***AlaGlnGlyGlnAla*****LeuAspLeuAsnArgLys***HisPheGlnLeuLeuPro 441

Db -----GAGAAATAGTTCTGTGTGACTTCTTGGAAAGCATCATCAATTTATTTTCA 13086

QY PheGlySerGlyArg***MetCysProGlnVal***LeuAlaThrSerGly***AlaThr 461

| | | | |
|--|------|--|------|
| Db | 1309 | TTTGGTCGGGAGAGAGATTGCTCGGAATGCTTTTGGTTTGGCAATGTTGACAA | 1368 |
| Qy | 462 | LeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeuGlyProGlnGlyGlnIle | 481 |
| Db | 1369 | CCATTACTGCAATTACTTTATCTTATCACTTCGATCGGAATCTC-----CCTAATGGCAAAAGT | 1422 |
| Qy | 482 | LeuIysGly***AspAlaIysValSerMetCnUGlnArgAlaGlyLeuThrValProArg | 501 |
| Db | 1423 | CACCAAAATTGTGAC-----ATGACGAGATGACCTGGAAATTTCGCAACANGA | 1470 |
| Qy | 502 | AlaHisSerLeuValCysVal 508 | |
| Db | 1471 | AAGGATGATCTTGTTTTGATT 1491 | |
| RESULT 9 | | | |
| US-09-142-108C-14 | | | |
| ; Sequence 14, Application US/09142108C | | | |
| ; Patent No. 6774285 | | | |
| ; GENERAL INFORMATION: | | | |
| ; APPLICANT: Bruggliera, Filippa | | | |
| ; APPLICANT: Holton, Timothy A. | | | |
| ; APPLICANT: Michael, Michael Z. | | | |
| ; TITLE OF INVENTION: GENETIC SEQUENCES ENCODING FLAVONOID PATHWAY ENZYMES | | | |
| ; TITLE OF INVENTION: AND USES THEREFOR | | | |
| ; FILE REFERENCE: 11658 | | | |
| ; CURRENT APPLICATION NUMBER: US/09/142,108C | | | |
| ; CURRENT FILING DATE: 1998-09-01 | | | |
| ; PRIOR APPLICATION NUMBER: PN8386 | | | |
| ; PRIOR FILING DATE: 1996-03-01 | | | |
| ; NUMBER OF SEQ ID NOS: 45 | | | |
| ; SOFTWARE: PatentIn Ver. 2.1 | | | |
| ; SEQ ID NO 14 | | | |
| ; LENGTH: 1748 | | | |
| ; TYPE: DNA | | | |
| ; ORGANISM: Rosa hybrida | | | |
| ; FEATURE: | | | |
| ; NAME/KEY: CDS | | | |
| ; LOCATION: (22)..(1563) | | | |
| US-09-142-108C-14 | | | |
| Alignment Scores: | | | |
| Pred. No.: 1,64e-75 Length: 1,748 | | | |
| Score: 623.00 Matches: 161 | | | |
| Percent Similarity: 48.73% Conservative: 89 | | | |
| Best Local Similarity: 31.38% Mismatches: 205 | | | |
| Query Match: 26.08% Indels: 58 | | | |
| Gaps: 3 Gaps: 16 | | | |
| Db: 3 | | | |
| US-09-857-581B-66 (1-521) x US-09-142-108C-14 (1-1748) | | | |
| Qy | 27 | LYSALALeuArgHis--LeuProAsnProSerPro***ProArgLeuProPheIle | 45 |
| Db | 88 | AAATCCCAACGCCACATCGCTCCCTCTCCCTCTGAGCCCAACCA---TGCCGGGTGTT | 144 |
| Qy | 46 | GlyHis***HisLeuLeuLysAspLysLeuLeuHisTyrAla***IleAspLeuSer | 64 |
| Db | 145 | GGCAACTTAACTCACTTG-----GGCCCTTCCGCAACACTCCATCGCGGAGTGGCG | 198 |
| Qy | 65 | LYSLVSHIAGLProLeuPheSer*****PheGlySerMetProThrValValAlaSer | 84 |
| Db | 199 | AGAAACACGGGCGGCTCTATGACCTCCGCTCGGCTACGTTGAGTAATCGTGGCGCA | 258 |
| Qy | 85 | ThrProGlnLeuPheLysLeuPheLeuGln*****GluAlaThrSerPhe***ThrArg | 104 |
| Db | 259 | TCAGCATCGGTGCGGCGCCAGTTCCTTGAGACTACAGAGCC---AATTCTTCAGCCGA | 315 |
| Qy | 105 | PheGlnThrSerAla***Arg***LeuThrTyrAsp-----ValAla*****Pro | 123 |
| Db | 316 | CGGCCCACTCGGCGGCCCAAGACCTCGCTTAACTACAGAGACTCGTTCGAGCGG | 375 |
| Qy | 124 | **GlyProTyrTyr***PheValArgLysLeuIleMetAsnAspLeu***AsnAlaThr | 143 |


```

Db      152 GGCACCTCCACTTCTGTGGGAGGCGTTCCCCAGACGTTTGAAGACATAGCCCA 211
Qy      66 lvsHsEgLYProLeuPheser*****PheGlySerMetProThyValAlaSerThr 85
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db     212 AAGTACGGGCGCGGTGGCGACGTCAGCTGGGAGAAAGTACCTGGGTGGTGTGTGTG 271
Qy      86 ProGluLeuPheLeuPheLeuGln*****GluAlaThrSerPhe***ThraCgPhe 105
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db     272 GCGGAGGACCGAGACGAGCGAGTGAAGGCTCTGAC---CCGAACCTCCCGACCGGTC 328
Qy     106 GlnThrSerAla***Arg***LeuThrTyAsp-----ValAla*****Pro*** 124
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db     329 GACGCGATCGGGTCCAGACCATGTGTACGACAAAGATGACATCTTCACGCCCTTAC 388
Qy     125 GlyProTyTrp***PheValAlaGlySLeuIleMetAsnAspLeu***AsnAlaThrThr 144
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db     389 AACGATCACTGGGCGCAGATCGGAGAGATCTGGCTGACAGAGCTGTGAGCCCGAAGAAC 448
Qy     145 ValAsn***LeuArgProLeuArgThrGlnGlnIleArgLys***LeuArg***MetAla 164
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db     449 GTTCAGTCTCTCGGATACATACAGGAGAGAGATGACGCGCTCATCCGCTGCTCGG 508
Qy     165 Gln***AlaGluAla***LysProLeuAsp***ThrGluLeuLeuLysTrp***Asn 184
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db     509 TCGTCGGGGGAGCG-----CCGTCGACGTGACGAGAGAGGTGTGGAAGATGTGTGT 562
Qy     185 SerThr***SerMetMet***LeuGly-----GluAlaGluGluIleArgAsp 200
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db     563 GTTCGTGTGCGAGGCGCGGCTTCGGGAGTGTCTCAGAGACGAGGTTCTGTGGCGAG 622
Qy     201 lIeAlaArgGluValLeuLysIle***GlyLysTrpSerLeuThrAspPheIle***Pro 220
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db     623 TTGGTAAAGAGATCGCTGGCATTTGGCGTCCGGGTTTACGTGGCGAT---CTTACCT 679
Qy     221 -----LeuLys***LeuLysValGlyLysTrpGluLysArgIleAspIle 236
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db     680 TCCTCATGGCTCTCAACCTGCTTAGCTTAACAAGTAC-----AGTTGACAGAGATG 733
Qy     237 LeuAsnLysPheAspProValValGluArgValIleLysLysArgArg***IleValArg 256
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db     734 CGCGCGCGCTCATACATCTTGATGGGTTCTCTGAGAGAGATGAG-----791
Qy     257 ArgArg***AsnGlyGlu*****GluGlyGlu***SerGlyVal***Leu---AspThr 275
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db     782 -----GAGAAGAAAGACGGCGAGTTTGCAGGACGACATCGTCAGCTT 826
Qy     276 LeuLeuGluPheAlaGluAspGluThr**GluIleLysIleThrLys*****Ile*** 295
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db     827 CTTTTCAGATGACAGAAAGGACGACGACATCAAAATTCCTTCTTCAATTCATCAG 886
Qy     296 GlyLeuValValAsp***PheSerAlaGly***AspSerThrAla*****ThrGluTrp 315
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db     887 GGTTCATTTTCACACCTTCTCCGGGAGCTGAACGTCCTTCGACGACCATCTCATGG 946
Qy     316 AlaLeuAlaGluLeuIleAsnAsnPro***ValLeu*****AlaArgGluGlu***Tyr 335
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db     947 GCGTTTCCGAATCTGATGAGGAATCCGCGAAGATGCCAAGTCCAGGCGGAGCTAAAG 1006
Qy     336 SerValValGlyLysAsp***LeuValAspGluValAspThrGlnAsnLeuProTyIle 355
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db     1007 GAGGCGCTCAAGGAAAGACAGTCGTGATTTGAGCAGAGTGCAGACGATCAAAATACCTG 1066
Qy     356 ArgAlaIleValLysGluThrPheArgMetHisProProLeuProValValLysArgLys 375
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db     1067 AGATCGGTGTTAAAGAGACTGAGGCTGACCCCTCCCTTCCATTAAATCCCAAGACAA 1126
Qy     376 Cys***GluGluCys***IleAsnGly***Val***ProGluGluAlaLeu*****Phe 395
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db     1127 TCACAGGAAAGAAATCCAGAGTTAAAGGATACACGATTCGCGCAAAACTAAGATCTTCATC 1186
Qy     396 AsnValTrpGlnValGly***Asp***LysTyTrpAspArgProSerGlu***ArgPro 415
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db     1187 AACGTCTGGGCTATCGGAAGGATCCCATATACCTGGGAAGATCCCGACACCTTCCGCGCT 1246

```

```

Qy     416 GluArgPheLeuGluThr**AlaGluGlyGluAla*****LeuAspLeuArgGly*** 435
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db     1247 GAGAGATTCGATGAGGTTTCCAGG-----GATTTCATGGGAAC 1285
Qy     436 HisPheGlnLeuLeuProPheGlySerGlyArg***MetCysProGlyVal***LeuAla 455
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db     1286 GATTTCGATTCATCCCATTCGCGGGGCGGTGCAAGAAATCTGCCCGGTTTACATTTCCGG 1345
Qy     456 ThrSerGly***AlaThrLeuAlaSerLeuIleGlnCysPheAspLeuGlnValLeu 475
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db     1346 CTGGCAATAGTTAGATCCCATTCGCGCAACTGCTTACACTTGCATCGAAATTG--- 1402
Qy     476 GlyProGlnGlyGlnIleLeuLysGly***AspAlaLysValSerMetGluGluArgAla 495
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db     1403 ---CCACAGGAATG-----ACTGATCCGACTTGGACATGACGAGACCCCA 1447
Qy     496 GlyLeuThrValProArgAlaHisSerLeuValCysValPro 509
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db     1448 GGTCTTCTGGGCGCAAAAAGAAAATGTTTGTCTGTGTTCCC 1489

RESULT 12
US-09-292-768-65
; Sequence 65, Application US/09292768
; Patent No. 6194185
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney B
; APPLICANT: Dupien, Shari L
; APPLICANT: Karp, Frank
; TITLE OF INVENTION: RECOMBINANT MATERIALS AND METHODS FOR THE PRODUCTION OF
; FILE REFERENCE: wsur13463
; CURRENT APPLICATION NUMBER: US/09/292,768
; EARLIER FILING DATE: 1999-04-14
; EARLIER FILING DATE: 1997-06-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 65
; LENGTH: 1762
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: computer-generated nucleic acid sequence encoding
; OTHER INFORMATION: limonene-6-hydroxylase
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1762)
; OTHER INFORMATION: computer-generated nucleic acid sequence encoding
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (20)..(1507)
US-09-292-768-65

Alignment Scores:
Pred. No.: 6,98e-75 Length: 1762
Score: 618.50 Matches: 146
Percent Similarity: 48.38% Conservative: 93
Best Local Similarity: 29.55% Mismatches: 214
Query Match: 25.89% Indels: 41
DB: 3 Gaps: 14

US-09-857-581B-66 (1-521) x US-09-292-768-65 (1-1762)
Qy     26 SerLysAlaLeuArgHisLeuProAsnProProSerPro**ProArgLeuProPheIle 45
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db     101 TCGAATTCACCAACAAACTA-----CCTCGAGGCGCT---CCGAAGCTGGCGGTGATC 151
Qy     46 GlyHis***HisLeuLeuLysAspLysLeuLeuHisTyAla***IleAspLeuSerLys 65
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db     152 GGCACCTCCACTTCTGTGGGAGGCGTTCCCCAGACGATGTTTGAAGACATAGCCCA 211

```

```

QY 66 LysHISgLYProleuPheSer*****PheGlySerMetProThrValValAlaSerThr 85
   |||
   |||
   |||
Db 212 AAGTACGGGCGCGGTGCGACGTGACGTGGAGAGTGTACTGTGCTGTGTGCTGTG 271
   |||
   |||
   |||
QY 86 ProGluLeuPheLeuPheLeuGln*****GluAlaThrSerPhe***ThrArgPhe 105
   |||
   |||
   |||
Db 272 GCGAGGACGAGGAGGCGGATGAGGCTGTGAC---CCGAACTTCGCCACCGGTTT 328
   |||
   |||
   |||
QY 106 GlnThrSerAla***Arg***LeuThrTyrAsp-----ValAla*****Pro*** 124
   |||
   |||
   |||
Db 329 GAGGCGATCGGCTCCAGACCATGTGTGACAAAGATGATCATCTTCACCCCTTAC 388
   |||
   |||
   |||
QY 125 GlyProTyrTrp***PheValArgLysLeuIleMetAsnAspLeu***AsnAlaThrThr 144
   |||
   |||
   |||
Db 389 AAGCATCACTGGCGCGCATGCGAGGATCTGCGTGCAGAGCTGTGAGCCCGAAGAAC 448
   |||
   |||
   |||
QY 145 ValAsn***LeuArgProleuArgThrGlnGlnIleArgLys***LeuArg***MetAla 164
   |||
   |||
   |||
Db 449 GTCAGGTCTTCGAGTACATMAAGCAGAGAGATCGAGCCTCATCCGCTGCGG 508
   |||
   |||
   |||
QY 165 Gln***AlaGluAla***LysProleuAsp***ThrGluGluLeuLeuLysTrp***Asn 184
   |||
   |||
   |||
Db 509 TCCTCGGGGGAGCG---CCGTCGACGTGACGAGAGAGGTGTGAAAGATGTGCTGT 562
   |||
   |||
   |||
QY 185 SerThr***SerMetMet***LeuGly-----GluAlaGluGluIleArgAsp 200
   |||
   |||
   |||
Db 563 GTCGTCTGTGCGAGGCGGCGTTCGGAGTGTCTGACAAAGACCGAGGTTGTCGGAG 622
   |||
   |||
   |||
QY 201 IleAlaArgLysValLeuLysIle***GlyGluTyrSerIleThrAspPheIle***Pro 220
   |||
   |||
   |||
Db 623 TTGGTGAAGAGTGTGCGATTTGCGCTCGCGGTTTACGTGCGGAGT---CTCTACCT 679
   |||
   |||
   |||
QY 221 -----LeuLys***LeuLysValGlyLysTyrGluLysArgIleAspPheIle 236
   |||
   |||
   |||
Db 680 TCCTCATGTCTCTCAACCTGCTTACGCTTGAACAGTAC-----AGTTCGACAGAGAT 733
   |||
   |||
   |||
QY 237 LeuAsnLysPheAspProValIleGluArgValIleLysLysArgArg***IleValArg 256
   |||
   |||
   |||
Db 734 CGCCGCGCTCATCATCTCTTGATGGGTCTGTGAGAGCATAG----- 781
   |||
   |||
   |||
QY 257 ArgArg***AsnGlyGlu*****GluGlyGlu***SerGlyVal***Leu---AspThr 275
   |||
   |||
   |||
Db 782 -----GAGAAGAAAGAGCGCGCATTTGAGCGAGCATCTGTGACGCTT 826
   |||
   |||
   |||
QY 276 LeuLeuGluPheAlaGluAspGluThr***GluIleLysIleThrLys*****Ile*** 295
   |||
   |||
   |||
Db 827 CTTTTCAGATGACAAAGGCGACGACATCAAAATCTCCATCTTCCATTCATGATCAG 886
   |||
   |||
   |||
QY 296 GlyLeuValValAsp***PheSerAlaGly***AspSerThrAla*****ThrGluTrp 315
   |||
   |||
   |||
Db 887 GGTTCATTTTCGACACCTTCTCCGCGGAGCTGAAAGCTTTCGACGACCATCTCATGG 946
   |||
   |||
   |||
QY 316 AlaLeuAlaGluLeuIleAsnAsnPro***ValLeu*****AlaArgGluGlu***Tyr 335
   |||
   |||
   |||
Db 947 GCGTTTCGAACTGATGAGATCCGCGCAAGATGCGCAAGTGCAGCGCGAGAGTAA 1006
   |||
   |||
   |||
QY 336 SerValValGlyLysAsp***LeuValAspGluValAspThrGlnAsnLeuProTyrIle 355
   |||
   |||
   |||
Db 1007 GAGCGCGCTCAAGGAAAGACAGCTGTGATTTGAGCGAGGTGCAAGACTTAAATACCTG 1066
   |||
   |||
   |||
QY 356 ArgAlaIleValLysGluThrPheArgMetHisProProleuProValIleValArgLys 375
   |||
   |||
   |||
Db 1067 AGATCGGCTTAAAGAGACTCTGAGGCTGCACCTCTTTCATTAATCCCAAGACAA 1126
   |||
   |||
   |||
QY 376 Cys***GluGluCys***IleAsnGly***Val***ProGluGlyAlaLeu*****Phe 395
   |||
   |||
   |||
Db 1127 TCCAGGGAAGATGCGAGTTTAAACGGTAAACAGATTCGCGCCAAATAGATCTTCAATC 1186
   |||
   |||
   |||
QY 396 AsnValITPGLInValGly***Asp***LysTyrITPAPAArgProSerGlu***ArgPro 415
   |||
   |||
   |||
Db 1187 AACGTCTGGCTATCGGAAGGATCCCAATATCTGGGAAGATCCCGACACCTTCGCGCTT 1246
   |||
   |||
   |||

```

```

QY 416 GluArgPheLeuGluThr***AlaGluGlyGluAla*****LeuAspLeuArgGly*** 435
   |||
   |||
   |||
Db 1247 GAGAGATTTCAGAGAGATTTCAGG-----GATTTCATGGGAAC 1285
   |||
   |||
   |||
QY 436 HisPheGlnLeuLeuProPheGlySerGlyArg***MetCysProGlyVal***LeuAla 455
   |||
   |||
   |||
Db 1286 GATTTCGAGTTTCATCCATTCGAGGCGGCTCAGAAATCTGCCGCTTACATTTCCGG 1345
   |||
   |||
   |||
QY 456 ThrSerGly***AlaThrLeuLeuAlaSerIleGlnCysPheAspLeuGlnValLeu 475
   |||
   |||
   |||
Db 1346 CTGGCAATGTGAGATCCCATTTGGGACACTGCTTACCACTTGCATCGAATTTG--- 1402
   |||
   |||
   |||
QY 476 GlyProGlnGlyGlnIleLeuLysGly***AspAlaLysValSerMetGluGluArgAla 495
   |||
   |||
   |||
Db 1403 ---CCAGAGAGATG-----ACTGATGCCACTTGGAGATGACGAGACCCCA 1447
   |||
   |||
   |||
QY 496 GlyLeuThrValProArgAlaHisSerLeuValCysValPro 509
   |||
   |||
   |||
Db 1448 GGTCTTTCGGGCCAAAGAAATATTTCTGTGTTCCC 1489
   |||
   |||
   |||

RESULT 13
US-09-351-229-3
/ Sequence 3, Application US/09351229
/ Patent No. 6380465
/ GENERAL INFORMATION:
/ APPLICANT: Barrett, Michael
/ TITLE OF INVENTION: Cytochrome P450 Enzymes and Related Compounds and
/ FILE REFERENCE: P-1049
/ CURRENT APPLICATION NUMBER: US/09/351,229
/ EARLIER FILING DATE: 1999-07-11
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 3
/ LENGTH: 1806
/ TYPE: DNA
/ ORGANISM: Zea mays
US-09-351-229-3

Alignment Scores:
Pred. No.: 8 51e-75 Length: 1806
Score: 618.00 Matches: 164
Percent Similarity: 50.40% Conservative: 90
Best Local Similarity: 32.54% Mismatches: 199
Query Match: 25.87% Indels: 52
DB: 3 Gaps: 13

US-09-857-581b-66 (1-521) x US-09-351-229-3 (1-1806)
QY 35 ProProSerPro***ProArgLeuProPheIleGlyHis***HisLeuLeuLysAspLys 54
   |||
   |||
   |||
Db 86 CCGCGCGGCGCCCAAGCA---TGGCGATCATCGGAGCTTAACCTCAG---GGCGAG 139
   |||
   |||
   |||
QY 55 LeuLeuHisTyrAla***IleAspLeuSerLysLysHisGlyProleuPheSer***** 74
   |||
   |||
   |||
Db 140 CTGCCCAACGCTTCATGAAGAGCTCTCCAAAGCGGTACGCTCGCTCATGCGAGCTTGG 199
   |||
   |||
   |||
QY 75 PheGlySerMetProThrValIleAlaIleThrProGluLeuPheLysLeuPheLeuGln 94
   |||
   |||
   |||
Db 200 TTGCGGCTGTGCTGTGTGTGCGCGCGCTCCGCGAGATGGCAAGACTTCTCTCAAG 259
   |||
   |||
   |||
QY 95 *****GluAlaThrSerPhe***ThrArgPheGlnThrSerAla***Arg***LeuThr 114
   |||
   |||
   |||
Db 260 ACCAAGCAGCGG---GGTTCTCCGACCGGCGAGGTTCAGATCGCGCAAGTACACCGCG 316
   |||
   |||
   |||
QY 115 TyrAsp---*****ValAla*****Pro***GlyProTyrTrp***PheValArgLys 133
   |||
   |||
   |||
Db 317 TACACATGCTCCGCGCTTCTGTGGGCTCTTTGAGCGGTACCTGCGCCGAGCAGCAGG 376
   |||
   |||
   |||
QY 134 LeuIleMetAsnAspLeu***AsnAlaThrThrValAsn***LeuArgProleuArgThr 153
   |||
   |||
   |||

```



```

Db      181 CTGCGCAGACCGCTGGCCAGCTGGCGAAGCAGTACGCCCAAGTGGCGCAGCTGGCAG 240
Qy      75 PheGlySerMetProThrValValAlaSerThrProGluLeuPheLeuPheLeuGln 94
Db      241 CTGCGGAGAGGTGTTCTCCGTGCTCTCTCTCCCGGAGGCGCAGAAAGAGGAGTGAAG 300
Qy      95 ****GluAlaThrSerPhe****ThrArgPheGlnThrSerAla****Arg****LeuThr 114
Db      301 CTGGTGAGAC---CCGGCTGCGCGGAGCCGTTCCAGAGCATCGGAGCAGAAATCATGTGG 357
Qy      115 TyrAsp---****ValAla****Pro****GlyProTyrTrp****PheValArgIys 133
Db      358 TACGACACACGACGACATCATCTTCAGCCCTACAGCGCTGACCTGGCGCGCAGATGCGGAG 417
Qy      134 LeuIleMetAsnAspLeu****AsnAlaThrThrValAsn****LeuArgProLeuArgThr 153
Db      418 ATCTGCGTCTCCAGCTCTCCAGCGCCGCAAGCTCCGCTCTTCGGCTTCATCAGGACAG 477
Qy      154 GlnGlnIleArgIys****LeuArg****MetAlaGln****AlaGluAla****LysProLeu 173
Db      478 GACGAGGTGTCGGCTCTCCGCTCCGACCTCGGCTCCGCGCGGCGGAGGCGCGTGG 537
Qy      174 Asp****ThrGlnIleLeuLeuLysTyrP****AsnSerThr****SerMetMet****LeuGly 193
Db      538 GACCTCAGCAGGAGCGATAGCAGCGCTGACGCTGCTCATCTGACAGGCGCGCGTGG 597
Qy      194 -----GluAlaGlnGlnIleArgAspIleAlaArgGluValLeuLysIle**** 209
Db      598 AGCGGTATCAGGAGCAGCAGAGAGCTGTGAGTGTGTGAAGGAGCGCTTCAGCATGGCG 657
Qy      210 GlyIuTyrSerLeuThrAspPheIle****ProLeuLys****Leu----- 224
Db      658 TCCGGGTTCAGAGCTCCGCGGACATGTTCCCTCCCAAGCTCCCACTTGGCTGCTGGTG 717
Qy      225 -----LysValGlyLysTyrGlnLysArgIleAspAspIleLeuAsnLysPheAsp 241
Db      718 AACAAAGACAAAGCTGTGAGAGATGCGCGCGCTGACGCGCATCTCGAGGCCATC--- 774
Qy      242 ProValValGluValGluValIleLysLysArgArg****IleValArgAspArg****AsnGly 261
Db      775 ---GTGAGAGACAAAGCTCAGAG--- 798
Qy      262 Glu*****GlnGlyGlu****SerGlyVal---****LeuAspThrLeuLeuGluPheAla 280
Db      799 -----AGCGCGAGCTTTGGCGCGGAGACATTAATGACGTAATCTTTAGATGAG 849
Qy      281 GluAspGluThr****GluIleLysIleThrLys****Ile****GlyLeuValValAsp 300
Db      850 AAGATAGACCATCAAAAGTCCCATCCATCACCAACGCGCATCAAAAGCTTCATCTTCGAC 909
Qy      301 ****PheSerAlaGly****AspSerThrAla****ThrGluTyrPalaLeuAlaGluLeu 320
Db      910 ACGTTCTCAGCGGAGCCGAGCATCATCAACCAACCATCTGTGGTGTGATGGCGAGGTG 969
Qy      321 IleAsnAsnPro****ValIleu*****AlaArgGlnGlu****TyrSerValValGlyLys 340
Db      970 ATGAGGAAATCCAGAGGTATGATGCGAAGGCGAGGCGGAGGAGAGCGCGCTGAAGGCG 1029
Qy      341 Asp****LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLys 360
Db      1030 AAGACGAGCTGGAGCTGACGACGAGCGTGAAGGCTTAATACATGAATTCGATGTGAG 1089
Qy      361 GlnThrPheArgMetHisProProLeuProValValLysArgLysCys****GlnGluLys 380
Db      1090 GAGAGCATGAGATGACCTCCCTCCGATCCGTTGATCCGAGATCAGAGAGAGAGATGC 1149
Qy      381 ****IleAsnGly****Val****ProGlnGlyAlaLeu*****PheAsnValTyrGlnVal 400
Db      1150 GAGGTCAACGGGTATACAGATCCGAATAAGGCGAAGATCATGATCAAGTGTGGTCCATG 1209
Qy      401 Gly****Asp****LysTyrTyrAspArgProSerGlu****ArgProGlnLysPheLeuLys 420
Db      1210 GGTAGGAATCTCTCTACTGGGAAAAAACCCGAGACCTTTTGGCCCGAAAGGTTT----- 1263

```

```

Qy      421 Thr****AlaGlnGlyGluAla*****LeuAspLeuArgLys****HisPheGlnLeuLeu 440
Db      1264 -----GACCAAGCTCTCAGAGGATTTTCATGAGAAACGATTTCCAGTTTCATC 1308
Qy      441 PropheGlySerGlyValArg****MetCysProGlyVal****LeuAlaThrSerGly****Ala 460
Db      1309 CCAATTGGAGCTGGAGAGAAAGAAATCTGCCCCGGTTTCAATTTGGCGTTGGCAATGTGAG 1368
Qy      461 ThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnVal-----LeuGlyPro 477
Db      1369 GTCCCATTTGGCAGAGCTTTCTTAACCATCTGACCTGGAAGTGGCGGAGAAATGAACCTT 1428
Qy      478 GlnGlyGlnIleLeuLysGly****AspAlaLysValSerMetGlnLysArgAlaGlyLeu 497
Db      1429 -----TCCGATATGACATGTTCTGAGCGAGAGGCGCTT 1461
Qy      498 ThrValProArgAlaHisSerLeuValCysValPro 509
Db      1462 ACCGGAATAAGAAAGAAACAATCTTCTACTGTTCC 1497

RESULT 15
US-09-292-768-3
; Sequence 3, Application US/09292768
; Patent No. 6194185
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney B
; APPLICANT: Lupien, Shari L
; APPLICANT: Karp, Frank
; TITLE OF INVENTION: RECOMBINANT MATERIALS AND METHODS FOR THE PRODUCTION OF
; FILE REFERENCE: wsur13463
; CURRENT APPLICATION NUMBER: US/09/292,768
; EARLIER FILING DATE: 1999-04-14
; EARLIER APPLICATION NUMBER: 08/881,784
; EARLIER FILING DATE: 1997-06-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1665
; TYPE: DNA
; ORGANISM: Mentha piperita
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (19)..(1518)
US-09-292-768-3

Alignment Scores:
Pred. No.: 1,21e-74 Length: 1665
Score: 616.50 Matches: 145
Percent Similarity: 47.76% Conservative: 90
Best Local Similarity: 29.47% Mismatches: 206
Query Match: 25.81% Indels: 51
DB: Gaps: 11

US-09-857-581b-66 (1-521) x US-09-292-768-3 (1-1665)
Qy      35 ProProSerPro****ProArgLeuProPheIleGlyHis****HisLeuLeuLysAspLys 54
Db      124 CTCTCGGAGCGCG---CCGAAGCTCCGCTGATCGGAGCATCTCCACCTCTTATGAGGGAG 180
Qy      55 LeuLeuHisTyrAla****IleAspLeuSerLysIleGlyProLeuPheSer***** 74
Db      181 CTGCGCAGCAGCGCGCTGCGCAGCGTGGCGAAGCATGACGCGCCAGTGGCGCAGCTGAG 240
Qy      75 PheGlySerMetProThrValValAlaSerThrProGluLeuPheLysLeuPheLeuGln 94
Db      241 CTGCGGAGAGGTGTTCTCCGTGCTCTCTCTCCCGGAGGCGCAGAAAGAGGAGTGAAG 300
Qy      95 ****GluAlaThrSerPhe****ThrArgPheGlnThrSerAla****Arg****LeuThr 114
Db      301 CTGGTGAGAC---CCGGCTGCGCGGAGCCGTTCCAGAGCATCGGAGCAGAAATCATGTGG 357

```

```

QY 115 TyrAsp-----ValAla*****Pro***GlyProHyTrp***PheValArgLys 133
Db 358 TACGACAAAGCAGCAGCATTCATCTTACAGCCCTTACAGCGTCGACTGGCGCCAGATGCGAAG 417
QY 134 Leu1IleMetAsnAspPheU***AsnAlaThrValAsn***LeuArgProLeuArgThr 153
Db 418 ATCTGGCTCTCCGAGCTCTCCAGCGCCGCGACGTCGCTCTTCCGGCTTCATCAGGCGAG 477
QY 154 GlnGlnIleArgLys***LeuArg***MetAlaGln***AlaGluAla***LysProLeu 173
Db 478 GACGAGGTGTCCGCTCTCCGCGCACCTCCGCTCTCCGCGCGCGCGGCGGCGCGCTG 537
QY 174 Asp***ThrGlnIleuLeuLysTrp***AsnSerThr***SerMetMet***LeuGly 193
Db 538 GACCTCAGGAGCGGATGCGAGCCTGACCTGCTCTCCATCTCTGCGAGGCGGCGCTTCGG 597
QY 194 -----GluAlaGlnIleArgAspIleAlaArgGluValLeuLysIle*** 209
Db 598 AGCGTATCAGGAGCAGCAGCAGGAGCTGTGTGAGCTGTGTAAGAGCGCCTCAGCATGGCG 657
QY 210 GlyIuTrpSerLeuThrAspPheIle***ProLeuLys***Leu----- 224
Db 658 TCCGGGTTCGAGCTCCGCGCATGTCCCTCTCCAGCTCTCAACTTGTCTGTCTGG 717
QY 225 -----LysValGlyLysTrpGluLysArgIleAspAspIleLeuAsnLysPheAsp 241
Db 718 AACCAAGACAAAGCTGTGAGAGATGCCGCCGCTGACGCCATCTCTCAGAGGCCATC--- 774
QY 242 ProValIleGluArgValIleLysLysArgArg***IleValArgArgArg***AsnGly 261
Db 775 ---GTGAGAGAGCACAAGCTCAAGAG----- 798
QY 262 Glu*****GlnGlnGlu***SerGlyVal-----LeuAspThrLeuLeuGluPheAla 280
Db 799 -----AGCGCGAGTTTGGCGGAGACATTAATGACGTACTCTTTAGATGACG 849
QY 281 GluAspGluThr***GlnIleLysIleThrLys*****Ile***GlyLeuValIleAsp 300
Db 850 AAGGATAGCCAGATCAAGTCCCATCACCAACAGCCCATCAAGCTTCATCTTCGAC 909
QY 301 ***PheSerAlaGly***AspSerThrAla*****ThrGlnTrpAlaLeuAlaGluLeu 320
Db 910 ACCTTCTCAGCGGAGCCGAGCATCATCAACACGACCTGTGGGTGATGGCGAGCTG 969
QY 321 IleAsnAsnPro***ValLeu*****AlaArgGlnGlu***TyrSerValIleGlyLys 340
Db 970 ATGAGGATTCAGAGGTGATGCGCAAGCCGAGCGGAGGTGAGAGCGCGCTGAAGGGG 1029
QY 341 Asp***LeuValAspGluValAspThrGlnAsnLeuProTyrIleArgAlaIleValLys 360
Db 1030 AAGACGAGACTGGAGCGTGCAGCGACGTGCAGAGCTTAAGTACATGAAATCGGTGTGAG 1089
QY 361 GluThrPheArgMetHisProProLeuProValValLysArgLysCys***GlnGluCys 380
Db 1090 GAGACGATGAGATGACACCTCCGATCCGTTGATCCGAGATCATGACAGAAAGATGC 1149
QY 381 ***IleAsnGly***Val***ProGlnGlyAlaLeu*****PheAsnValTrpGlnVal 400
Db 1150 GAGGTCAACCGGTACACGATTCGCAATATAGGCCAAGATCATGATCACTGTGTGCATG 1209
QY 401 Gly***Asp***LysTrpTrpAspArgProSerGlu***ArgProGluArgPheLeuGlu 420
Db 1210 GGTAGGATCTCTCTCTATGTGGAAGAACCCGAGACCTTTGGCCCGAAGAGTTT----- 1263
QY 421 Thr***AlaGlnGlyGluAla*****LeuAspLeuArgGly***HisPheGlnLeuLeu 440
Db 1264 -----GACCAAGTCTCGAGGAGATTTCATGGAAGAAAGATTTTCAGATTTCATC 1308
QY 441 ProPheGlySerGlyArg***MetCysPProGlyVal***LeuAlaTrpSerGly***Ala 460
Db 1309 CCAATTTGAGCTGTGAAGAAAGATCTGCCCCGCTTGTGAATTCGGGTGGCAATGTGTGAG 1368
QY 461 ThrLeuLeuAlaSerLeuIleGlnCysPheAspLeuGlnVal-----LeuGlyPro 477

```

```

Db 1369 GTCCATTGGCACAGCTTCTTTACCACTTTCGACTGGAAGTTGGCGGAAGAAATGAACCTT 1428
QY 478 GlnGlyGlnIleLeuLysGly***AspAlaLysValSerMetGlnGluArgAlaGlyLeu 497
Db 1429 -----TCCGATATGACATGTCTGAGGCGAGAGGCCCTT 1461
QY 498 ThrValProArgAlaHisSerLeuValCysValPro 509
Db 1462 ACCGGAATAGAAAGAACATCTTCTACTGTTCCC 1497

```

Search completed: December 22, 2005, 00:21:08
Job time : 291 secs